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Listing first 45 summaries
                                                                                                                                                                                                                                                                          Result
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                                                                                                                                                                                                                                                                            Score
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Match
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Copyright (c) 1993 - 2000 Compugen Ltd.
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A_Geneseq_1101:*

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	N-terminal peptide	NTS
	de fragment. 9; vaccine;	Arabidopsis thalia C glutamicum prote Human protein seque C glutamicum prote protein seque C glutamicum protein seque C glutamicum protein sequence Arabidopsis thalia consensus sequence Capaicum annuum ly amino acid sequenc Amino acid sequenc Amino acid sequenc Serine protease in serine s

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                 Disclosure;
                               Antigenic Pseudomonas aeruginosa pand/or diagnosis of P. aeruginosa against P. aeruginosa -
                                                                            WPI; 2001-080988/09.
                                                                                                                  (PROV-) PROVALIS UK LTD
                                                                                                                                        01-JUL-1999;
                                                                                                                                                         03-JUL-2000; 2000WO-GB02554.
                                                                                                                                                                               11-JAN-2001.
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                                                                                                                                                                                                                              Misc-difference
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                                                                                                                                                                                                                                                                                                                     diagnosis; detection; infection;
                                                                                                                                                                                                                                                                                                                                   Pseudomonas
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                                                                                                                                                                                                                                                                                                                                                                                             AAB69062;
                                                                                                                                                                                                                                                                                                                                                                                                            AAB69062 standard; peptide; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein antigen; Pa60. This irragment could be detection of P. aeruginosa by forming complexes with specific antibodies, particularly in patients with cystic fibrosis (by analysis of mucus, e.g. in saliva), or in vaccines or immunogenic compositions to treat or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This peptide is the N-terminal fragment of protein antigen, Pa60. This fragment could
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein antigen from Pseudomonas aeruginosa and its antigenic fragments - useful diagnostically to detect specific antibodies, particularly in patients with cystic fibrosis, and as vaccines
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18; Conser
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                Page 2;
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a infections and f
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                                                                                            Peek K,
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1.7e-06;
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                                                                                         Sizer PJH,
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                                                in the detection
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The present invention describes antigenic Pseudomonas aeruginosa

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RESULT
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Best Local :
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07-MAY-1999;
11-MAY-1999;
14-MAY-1999
18-MAY-1999
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23-MAR-1999;
25-MAR-1999;
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05-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                             EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                              Protein identification hybridisation assay;
                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 35912.
                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                    termination sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins (P1). The P. aeruginosa proteins have antibacterial activity and can be used in vaccines and as antagonists. The proteins or their fragments, or antibodies are useful in the detection and/or diagnosis inducing an immune response against p. aeruginosa infection. An agent function or expression of P1 are useful in the derivine and capable of antagonising, inhibiting or otherwise interfering with the medicament for the treatment or prophylaxis of P. aeruginosa infections. The present sequence represents a probable P. aeruginosa protein N-terminal peptide sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-OCT-2000
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sation assay; genetic mapping; gene expression control; promoter
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18; Conserv
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     99US-0132863.
99US-0134256.
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99US-0132487.
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99US-0123180.
99US-0123548.
99US-0125788.
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99US-0132048.
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990S-0127462
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PR 22-00 PR 25-00 PR 25-00 PR 25-00	PR 21-0C PR 21-0C PR 21-0C PR 21-0C PR 22-0C	PR 18-0C PR 21-0C PR 21-0C	PR 14-0C PR 14-0C	PR 14-0C	PR 13-0C'	PR 08-007 PR 12-007	PR 06-0C1	PR 04-001 PR 05-001	PR 28-SEF	PR 23-SEF	PR 16-SEP PR 20-SEP	PR 13-SEP	PR 07-SEP	PR 30-AUG	PR 27-AUG	PR 27-AUG	PR 25-AUG	PR:	PR 20-AUG	PR 18-AUG	PR 17-AUG	PR 13-AUG	PR 12-AUG-	PR 10-AUG-	PR 09-AUG-	PR 06-AUG-	PR 05-AUG-	PR 04-AUG- PR 05-AUG-	PR 03-AUG- PR 04-AUG-	PR 02-AUG-	200 200
22-003 22-003 25-003 25-003	21-001 21-001 21-001 21-001 21-001	18-007 21-007 21-007	14-0CT	14-0CT	13-OCT	12-0CT	06-0CT	04-0CT 05-0CT	28-SEP	23-SEP	16-SEP 20-SEP	13-SEP-	07-SEP-	30-AUG-	27 - AUG -	27 - AUG -	25-AUG-	PR 23-AUG-	20-AUG- 20-AUG-	18-AUG- 20-AUG-	17-AUG-	13-AUG-	12-AUG-	11-AUG-	09-AUG-	06-AUG-1	05 - AUG - 1	04 - AUG - 1 05 - AUG - 1	04-AUG-1	02-AUG-1	02-AUG-1
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                                                    The present sequence represents a deoxyribokinase enzyme. This enzyme is involved in the biosynthesis of deoxyribonuclosides, and is used in the method of the invention. The specification describes a method for the in vitro enzymatic synthesis of deoxyribonucleosides. The method comprises reacting deoxyribose 1-phosphate and a nucleobase to form a deoxyribonucleoside and an inorganic phosphate. Enzymes which to grave the method of the invention include thymidine phosphopentose mutase, phosphopentose aldolase, fructose 1,6-diphosphate aldolase, deoxyribokinase, and nucleoside 2-deoxyribosyltransferase.
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- PX 20-	PR 20-	PR 17-	PR 16-	PR 13-	PR 12-	PR 11-	DR 10-	PR 09-	PR 06-	PR 06-	מק מקי	DR 04	PR 04	PR 03	PR 02	PR 02	PR 28	PR 27	PR 27	PR 26	PR 23	- PR 23	PR 22	PR 22		PR 21	PR 21	PR 20	PR 20	PR 19	PR 15	PR 10	PR 19	PR 1	PR 1	PR 1	PR 1	PR 1	PR 0	יא ס	PR. 0	- PR 0	PR 2	PR 2	PR 2	PR	PR J	PR 1	PR	PR	DR .
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Matches 9
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23-AUG-1999;
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  18-OCT-2000
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                                                                                                                                                   Score 44; DB pred. No. 15; 2; Mismatches
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05-MAR 1999

09-MAR 1999

23-MAR-1999

24-MAR-1999

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23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

24-MAY-1999

06-MAY-1999

06-MAY-1999

11-MAY-1999

11-JUN-1999

11-JUN-1999
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PR PR PR PR PR PR PR PR PR PR

> 24-JUN-1999; 28-JUN-1999; 29-JUN-1999; 30-JUN-1999; 01-JUL-1999;

14-JUL-1999; 15-JUL-1999; 16-JUL-1999;

16-JUL-1999

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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RESULT
AAG43602
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Matches 9
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                                                      EP1033405-A2
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23-JUN-1999
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14 - MAY - 1999

18 - MAY - 1999

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27 - MAY - 1999

28 - MAY - 1999

20 - JUN - 1999

01 - JUN - 1999

04 - JUN - 1999
                                                                                                                                                                                                                                                                                                                                                                                                                               30-APR-1999
30-APR-1999
04-MAY-1999
05-MAY-1999
06-MAY-1999
06-MAY-1999
07-MAY-1999
11-MAY-1999
14-MAY-1999
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10-JUN-1999
                                                                                                                                                                                                                                                                            10-JUN
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06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-FEB-1999;
05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-APR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .999;
99US-0121825.
99US-0123180.
99US-0123180.
99US-0123180.
99US-0123180.
99US-0126786.
99US-0126786.
99US-0126786.
99US-012871.
99US-013049.
99US-013049.
99US-0132048.
99US-0132487.
99US-0134218.
99US-013428.
99US-0134219.
99US-013428.
99US-013945.
99US-013945.
99US-013945.
99US-013945.
99US-013946.
99US-014082.
99US-0141287.
99US-0141287.
99US-014128.
99US-01428.
99US-01428.
99US-01428.
99US-01428.
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Best Local S
Matches 9
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04-OCT-1999
05-OCT-1999
06-OCT-1999
06-OCT-1999
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29-OCT-1999
29-OCT-1999
                          06-OCT-1992;
22-OCT-1992;
30-DEC-1992;
01-JUN-1993;
                                                                                                                                                Human immunodeficiency virus; HIV; antigen; detection; diagnosis; retrovirus; vaccine; lymphocyte; reverse transcriptase.
                                                                                                                                                                                                                                    AAR51691
                                                                                                                                                                           HIV-type virus MVP5180/91 gag
                                                                                                                              HIV-type virus
                                                                                                                                                                                                07-NOV-1994 (first entry)
                                                                                                                                                                                                                   AAR51691;
                                                                                           13-APR-1994.
                                                                                                              EP591914-A.
                                                                         05-OCT-1993;
                                                                                                                                                                                                                                                                                  (BEHW ) BEHRINGWERKE AG.
                                                                                                                                                                                                                                                                                            2 EEKTPLTTAAXAPVVXNA
                                                                                                                                                                                                                                                                                                                        Similarity 50.0
9; Conservative
                                                                                                                                                                                                                                    standard; Protein; 498
                                                                                                                                                                                                                                                                                                                                                             99US-0156596.
99US-0157753
99US-0157865.
99US-0158232
99US-0158232
99US-0159294.
99US-0159294.
99US-0159330.
99US-0159331.
99US-0159331.
99US-015938.
99US-015938.
99US-0160767.
99US-0160767.
99US-0160788.
99US-0160788.
99US-0160788.
99US-0160789.
99US-0160814.
99US-0160980.
99US-0160980.
99US-0161406.
                            92DE-4233646.
92DE-4235718.
92DE-4244541.
93DE-4318186.
                                                                                                                                MVP-5180/91 (ECACC V92092318).
                                                                           93EP-0116058
                                                                                                                                                                                                                                                                                                                                   51.9%;
                                                                                                                                                                                                                                                                                                         19
                                                                                                                                                                                                                                                                                      308
                                                                                                                                                                                                                                                                                                                         ; Score 42; DB;
; Pred. No. 25;
1; Mismatches
                                                                                                                                                                               protein (cloned).
                                                                                                                                                                                                                                         AA.
                                                                                                                                                                                                                                                                                                                                              21;
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                                                                                                                                                                                                                                                                                                                                              Length 332;
                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                 0
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990S-0142977.
990S-014324.
990S-014325.
990S-0144085.
990S-0144331.
990S-0144333.
990S-0144333.
990S-0144333.
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990S-0144335.
990S-01445085.
990S-0145086.
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990S-0145086.
990S-0145218.
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990S-0145218.
990S-0145218.
990S-0145286.
990S-0145286.
990S-0147933.
990S-0151083.
990S-0151083.
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990S-0151083.
990S-0151083.
990S-0151083.
990S-0151083.
990S-0153070.
990S-0154039.
990S-0155438.
990S-0155438.

12-JUL-1999;
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16-JUL-1999;
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16-JUL-1999;
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29-JUL-1999;
20-AUG-1999;
20-AUG-1999;
20-AUG-1999;
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21-AUG-1999;
21-AU

18-AUG-1999;
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30-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-SEP-1999;
11-SEP-1999;
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13-SEP-1999;
13-SEP-1999;
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23-SEP-1999;
23-SEP-1999;
23-SEP-1999;
24-SEP-1999;
24-SEP-1999;
24-SEP-1999;

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RESULT 11
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Best Local :
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                                                                                                                      01-JUN-1993;
06-OCT-1992;
22-OCT-1992;
     New HIV-type retrovirus and corresponding
                                  WPI; 1999-072878/07.
                                                                                                              30-DEC-1992;
                                                                                                                                                                       05-OCT-1993;
                                                                                                                                                                                                  13-JAN-1999.
                                                                                     (DADE-) DADE
                                                                                                                                                                                                                        EP890642-A2
                                                                                                                                                                                                                                            Human immunodefictency virus
                                                                                                                                                                                                                                                                    HIV-type retrovirus; detection; antibody;
                                                                                                                                                                                                                                                                                                       HIV isolate 5180 gag
                                                                                                                                                                                                                                                                                                                                                              AAW93076;
                                                                                                                                                                                                                                                                                                                                   19-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MVP-5180/91 has been isolated from peripheral lymphocytes of a patient, from the Cameroons, with immune deficiency. It grows in the same human cells as HIV-1; like HIV it produces an Mg-dependent reverse transcriptase (RT), although this is 3 to 7 kD smaller in Western blots than the enzyme from HIV-1 or -2. It is less reactive than HIV-1, but more reactive than HIV-2, against p24-specific antibodies and its gp41 transmembrane protein reacts with antibodies in sera of African patients but not (or only weakly) with sera of
                                                                                                                                                                                                                                                                                                                                                                                 AAW93076 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The virus consists of RNA in a peg-shaped core made of p24 subunits surrounded by an outer core of p17 and then a glycoprotein envelope which, apart from host-cell derived lipids, comprises gp41 and envelope protein gp120 (which can bind to the CD4 receptor). Related viruses have at least 75% homology over the entire genome with max. differences for the various regions LTR and NEF 10%, POL 12%, GAG 14%, VIF 15% and ENV 22%.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           119 eetsprqtsqnypivtna 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig|7; 73pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New HIV-type immune deficiency virus ECACC V 92092318 -deriv. cDNA or antigens, useful for diagnosing retrovirg infections and vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ58974
                                                           Eberle J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        498 AA;
                                                                                  BEHRING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eberle
                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                        93DE-4318186.
92DE-4233646.
92DE-4235718.
92DE-4244541.
                                                                                                                                                                      93EP-0116058
                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J,
                                                                                  MARBURG GMBH
                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                             MVP\text{-}5180/91; <code>ECACC V 92092318; antigen; assay kit; immune deficiency; vaccine.</code>
                                                         Guertler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gurtler LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         German
                                                                                                                                                                                                                                                                                                                                                                                498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ω
                                                        LG,
                                                                                                                                                                                                                                                                                                                                                                               AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                        Hauser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hauser H-P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
84;
      CDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                    Knapp
  recombinant DNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          retroviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Knapp S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG39690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
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         11-MAY-1999;
14-MAY-1999;
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Ъ Qy

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Query Match 49.4
Best Local Similarity 44.4
Matches 8; Conservative
                                                                                           05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
                                                                                                                                                                                                               04-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                16-APR-1999;
19-APR-1999;
                                                                                                                                                                                                                                                                   30-APR-1999
                                                                                                                                                                                                                                                                                         28-APR-1999
                                                                                                                                                                                                                                                                                                                              23-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                        21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-FEB-1999;
05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAR-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      termination sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG39690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes the isolation of a novel HIV-type retrovirus called MVP-5180/91 (ECACC V 92092318). Antigens produced from this produce to the season of the seas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG39690 standard; Protein; 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 eetsprqtsqnypivtna 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigen - used
deficiency and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    498
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99US-0132048

99US-0132484

99US-0132485

99US-0132485

99US-0132486

99US-0132487

99US-0132863

99US-0134256

99US-0134258

99US-0134218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fig 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0127462:
99US-0128234.
99US-0128714.
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99US-0130077
                                                                                                                                                                                                                                                                                                                       99US-0130891
                                                                                                                                                                                                                                                                                                                                                      99US-0130510
                                                                                                                                                                                                                                                                                                                                                                           9908-0130449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0126264
99US-0126785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0123548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  990S-0121825
990S-0123180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for detect:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detecting retro-viruses that cause prepare vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49147.
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Best Local
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                    Novel polynucleotides derived from Coryneform bacteria, for identif mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-376931/40.
N-PSDB; AAH67128.
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Tateishi N,
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25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
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8; Conserv
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2000JP-0159162.
2000JP-0280988.
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Senoh A, Ik
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66.78;
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da M,
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Pred. No. 28;
0; Mismatches
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Ozaki A;
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28;
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analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described
                                                                                                                                                                                                                      The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. The are useful for identifying the mutation point of a gene derived from a
                                                                                                                                                                                                     mutant of coryneform bacterium, measuring expression amount and
                                                                                                                                                                                                                                                                                                5663; 246pp + Sequence Listing; English.
                                                        for this patent did not form obtained in electronic format
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oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH3633 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                             the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the
                                                                                                                                                                                                                                                                                                                                    The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                     sequence and an oligonucleotide comprising a sequence complementary to polynucleotide which comprises a 3'-end sequence, where the
                                                                                                                                                                                                                                               complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                     to the complementary strand of a polynucleotide which comprises one
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; SEQ ID 15864;
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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T, Wakamatsu
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66.7%;
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A, Nagai F
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in the exemplification of the invention. Note: The sequence data for this patent specification, but was obtained in elect. European Patent Office.

Claim

17;

SEQ ID

NO:

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Gaps

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RESULT 15
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Best Local Similarity
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of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C glutamicum protein fragment SEQ ID NO: 5209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG91455 standard; Protein; 261 AA.
                      The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These sequences from identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing manno acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162;
03-AUG-2000; 2000JP-0280988!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1108790-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium glutamicum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JUN-2001.
                                                                                                                                                                                                                                                                                                                                              WPI; 2001-376931/40.
N-PSDB; AAH66674.
                                                                                                                                                                                                                                                                                                                                                                                          Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                  (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                      Claim 17; SEQ ID NO: 5209; 246pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                        Mizoguchi H, Ando S, Hayashi M,
Senoh A, Ikeda M, Ozaki A;
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39.38;
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Pred. No.
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78;
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Query Match Best Local Similarity

46.98; 70.08;

Score 38; pred. No.

90;

22;

Length 261;

Sequence

261 AA;

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                             Matches
149 plttasaspv 158
             6 PLTTAAXAPV 15
                             7;
                             Conservative
                              2;
                              Mismatches
                                1;
                                Indels
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Search completed: February 28, Job time: 75 sec 2002, 11:34:39

Fri

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Title:
Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ainimum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
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length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212252 seqs, 22503292 residues
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Match Length
                                                                                                                                                                                                                                                                                                                 50.6
49.4
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/cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/1aa/backfiles1.pep:*
 182
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            US-08-194-338-12
US-08-470-202-59
US-08-471-770-59
US-08-468-059-59
US-08-679-635A-4
US-08-68-34-173-2
US-08-943-173-16
US-08-943-173-2
US-08-943-173-2
US-08-945-476-19
US-08-945-476-19
US-08-945-476-19
US-08-117-257-48
US-08-119-262B-6
US-08-119-262B-6
US-08-119-262B-6
US-08-119-262B-6
US-08-119-262B-11
US-09-91-219-24
US-09-93-318A-4
US-09-99-32-318-4
US-09-99-260-4
US-09-99-260-4
US-09-99-260-4
US-09-99-260-4
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21.507 Million cell updates/sec
    Sequence 59, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 16, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 142, Appl
Sequence 142, Appl
Sequence 142, Appl
Sequence 4, Appl
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Sequence
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RESULT 1
US-08-194-338-12
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                               HYPOTHETICAL: 1
ANTI-SENSE: NO
FRAGMENT TYPE:
US-08-194-338-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Venter, John C.
APPLICANT: Venter, Claire M.
APPLICANT: McCombie, William R.
APPLICANT: MCCOmbie, William R.
APPLICANT: MCCOMBIE, COTOPAMINE RE
TITLE OF INVENTION: OCTOPAMINE RE
TUBBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                              NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH101.001DV1
REFERENCE/DOCKET NUMBER: NIH101.001DV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8350
TELEPAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER:
POPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,174
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                  STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
CITY: N
STATE:
                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSEE: Knobbe, Martens, olson and Bear
T: 620 Newport Center Drive, Sixteenth Floor
Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                 92660
                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CA
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                                                                                                                                       788 amino acids
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                                                                     . protein
                                                                                                     linear
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08-FEB-1994
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4551
4613
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50.6%;
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US-09-117-257-21

US-08-945-476-21

US-09-117-257-52

US-09-117-257-52

US-07-927-071-2

US-08-446-9194-2

US-08-446-9194-2

US-08-450-360-4

US-08-450-360-3

US-08-968-563-16

US-08-968-563-16

US-08-969-683A-16

US-08-127-499A-8

US-08-127-499A-8
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US-09-105-537-31
US-09-105-537-6
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 Score 41;
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     ВС
     <u>ب</u>
..
    Length 788;
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Sequence
Sequence
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32, Appl 2
22, Appl 2
21, Appl 2
22, Appl 2
23, Appl 3
24, Appl 3
27, Appl 3
28, Appl 3
39, Appl 3
30, Appl 3
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35, Appl 3
36, Appl 3
37, Appl 3
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Query Match

52.9%;

Pred. No. 40;

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Query Match
Best Local Similarity
Thehes 8; Conserve
                                                                                                                                 MOLECULE TYPE: protein FRAGMENT TYPE: internal US-08-470-202-59
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/132,653
FILING DATE: 05-OCT-1993
APPLICATION NUMBER: DE P 42 33 646.5
FILING DATE: 06-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 35 718.7
FILING DATE: 22-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 35 718.7
FILING DATE: 30-DEC-1992
APPLICATION NUMBER: DE P 42 44 541.8
FILING DATE: 30-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATA:
APPLICATION NUMBER: DE P 42 18 541.8
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                                                                                                                                                                                                                        TELEFAX: 202-408-4400
INFORMATION FOR SEQ | ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 59
Patent No.
                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 37,096
REFERENCE/DOCKET NUMBER: 054
TELECOMMUNICATION, INFORMATION:
TELEPHONE: 2021408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: DE P 43 18 186.4
FILING DATE: 01-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn ReloCURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hauser, Hans-Peter TITLE OF INVENTION: Retrovirus TITLE OF INVENTION: Use NUMBER OF SEQUENCES: 63
                                                                                                                                                                                                                                                                                                                                           NAME: Michael J. Blake
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Finnegan, Henderson,
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
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                                                                                                                                                                                             amino acid
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                                                                                                                                                                                                          498 amino acids
                                              Conservative
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Knapp, Stefan
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                                                            44.48;
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                                                          Score 40; DB 1; Length 498; Pred. No. 35;
                                                                                                                                                                                                                                                                                                        05495-0001-00000
                                       Mismatches
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                                   Indels
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                               Gaps
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                                                                                                                     70POLOGY: 11; MOLECULE TYPE: FRAGMENT TYPE: US-08-471-770-59
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                                                     Query Match
Best Local :
                                        Matches
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                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: DI
FILING DATE: 22-OCT-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE
FILING DATE: 30-DEC-19
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                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
LENGTH: 498 amino acid
                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                             FILING DATE: 01-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Carol P. Einaudi
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                             FILING DALL.
PRIOR APPLICATION DATA:
DE P 43
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/132,653
FILING DATE: 05-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Knapp, Ste
APPLICANT: Hauser, He
TITLE OF INVENTION: I
TITLE OF INVENTION: (
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: LIC
CITY: Washington
CTATE: D.C.
                                                                                                                                                                                          TYPE:
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2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 06-JUNCLASSIFICATION: 439
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                                     Similarity 44.48;
8; Conservation
                                                                                                                                                                                 amino acids
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5770427
                                 Conservative
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1300 I Street, N.W.
                                                                                                                                                                    Linear
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VENTION: Retrovirus from the HIV Group and Its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eberle, Josef
Brunn, Albrecht v.
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                                                                                                                                   protein
internal
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22-OCT-1992
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                                                                                                                                                                                                                                                                                                                 32,220
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                                                                                                                                                                                                                                   59:
                            3; Mismatches
                                        Score 40; DB 1; Length 498; Pred. No. 35;
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                        7; Indels
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LENGTH:

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119 EETSPROTSQNYPIVTNA 136

US-08-468-059-59

Sequence 5

5840480

Application US/08468059

GENERAL INFORMATION:

APPLICANT:

Guertler, Lutz G. Eberle, Josef Brunn, Albrecht v. Knapp, Stefan

APPLICANT:

PPLICANT:

Hauser, Hans-Peter

Retrovirus from the HIV Group and Its

TITLE OF INVENTION: Use NUMBER OF SEQUENCES: 63

LE OF INVENTION:

CORRESPONDENCE ADDRESS:

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; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-468-059-59
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                                             Matches
                                                             Query Match
Best Local
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CURRENT APPLICATION DATA
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: L
FILING DATE: 01-JUN-1
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 01
FILING DATE: 05-OCT-1993
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APPLICATION NUMBER: 1
FILING DATE: 22-OCT-1
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                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acid
                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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FILING DATE: 06-OCT-1992
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                                                                                                                                                                                                                                                                                                      NAME: Carol P. Einaudi
REGISTRATION NUMBER: 32,220
                                                                                                                                                                  TOPOLOGY:
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                                             Local Similarity
es 8; Conserv
EEKTPLTTAAXAPVVXNA 19
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                                                                                                                                                                                                                                                                                                                                                                                              NUMBER: DE P 42 44 541.8
30-DEC-1992
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01-JUN-1993
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                                                                                                                                                     protein
                                                             49.48;
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                                                Score 40; DB
Pred. No. 35;
3; Mismatches
                                                                DB 2;
35;
                                                                                Length 498
                                                   Indels
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RESULT 5
US-09-109-916-59
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                                                                                          ; ORGANISM: Human immunodeficiency virus US-09-109-916-59
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Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                               SEQ ID NO 59
LENGTH: 498
                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: DE P 42 33 646.5 EARLIER FILING DATE: 1992-10-06 EARLIER FILING DATE: 1992-10-22 EARLIER FILING DATE: 1992-10-22 EARLIER APPLICATION NUMBER: DE P 42 34 541.8 EARLIER FILING DATE: 1992-12-30 EARLIER FILING DATE: 1992-12-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Brunn, Albrecht V.
APPLICANT: Knapp, Stefan
APPLICANT: Hauser, Hans-Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Guertler,
                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: DE P 43 18 186.4 EARLIER FILING DATE: 1993-06-01 NUMBER OF SEQ ID NOS: 67
                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND FILE REFERENCE: 05495.0001-04 CURRENT APPLICATION NUMBER: US/09/109,916 CURRENT FILING DATE: 1998-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Eberle, Josef
                                                                                                                                                                                        SOFTWARE:
                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 EETSPROTSONYPIVTNA 136
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                                                                                                                                                                                       PatentIn Ver. 2.0
     Conservative
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                       49.48;
     Score 40; DB Pred. No. 35; Mismatches
                       DB
35;
                                               4.
                                             Length 498
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             Indels
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Gaps

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Š US-08-624-125-20 Sequence 20, Application US/08624125 Patent No. 5744341 GENERAL INFORMATION:
APPLICANT: CUNNINGHAM JR., FRANCIS X.
APPLICANT: SUN, ZAIREN
TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND
TITLE OF INVENTION: METABOLISM AND A SYSTEM FOR SCREENING SUCH GENES
NUMBER OF SEQUENCES: 21 COMPUTER: IBM PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pstebtin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/624,125
FILING DATE: 29-MAR-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ANAMER AFFILED CTEVEN B COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk CORRESPONDENCE ADDRESS: 119 EETSPROTSONYPIVTNA 136 CITY: ARLINGTON ADDRESSEE: OBLON ADDRESSEE: P.C. STREET: 1755 S. 2 EEKTPLTTAAXAPVVXNA 19 COUNTRY: UZIP: 22202 NAME: KELBER, STEVEN B. REGISTRATION NUMBER: 30,073 ٧A USA OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT JEFFERSON DAVIS HIGHWAY, SUITE 400 Version #1.30

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US-08-679-635A-4
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                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BatentIn Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/679,635A
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                                              Query Match
Best Local (
                                Matches
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                                                                                                                                                                                                                        TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                     NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION 'INFORMATION:
TELEPHONE: 2014487 5800
                                                                                                                      MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tomasz, Alexander
APPLICANT: Delencastre, Herminia
TITLE OF INVENTION: AUXILIARY GENES AND PROTEINS OF
TITLE OF INVENTION: METHICILLIN RESISTANT BACTERIA AND ANTAGONISTS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: David.A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                              Local Similarity hes 8; Conserv
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                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/01
FILING DATE: 10-JUL-1996
CLASSIFICATION: 435
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                                                                                                                                                                STRANDEDNESS:
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STREET: Floor |
CITY: Hackensack
8 TTAAXAPVVXNA 19
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                                                                                                                                                                                                ENGTH:
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STRANDEDNESS: 'single
TOPOLOGY: linear
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                                                                                                                                                                                amino acid
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                                                                                                                                                                                             463 amino acids
                            Conservative
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                                         45.7%;
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72.78;
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                                        Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                     600-1-141
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                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.30
                                         1e+02;
                                                      DB 2;
                                                    Length 463;
                        Indels
                      0,
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US-08-943-173-16
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Matches
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; MOLECULE TYPE: US-08-943-173-8
                            GENERAL INFORMATION:
APPLICANT: Wang, Chang
APPLICANT: Shen, Fan
APPLICANT: Chen, Pei D
TITLE OF INVENTION: PE
TITLE OF INVENTION: FR
TITLE OF INVENTION: FO
TITLE OF INVENTION: DI
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-943-173-8
                                                                                                                                                                                Sequence 16, Application US/08943173 Patent No. 6048538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                  CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Lin, Maria C.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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nes 8; Conserv
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REGISTRATION NUMBER: 29
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  382 TTAAAAPLVQTA 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                          5 ERQKPLKVKAKAPVV 19
                                                                                                                                                                                                                                                                                                       2 EEKTPLTTAAXAPVV 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8, Application US/08943173
5. 6048538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10154-0053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        345 Park Avenue
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen, Pei De
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shen, Fan
Maria C.H. Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maria C.H. Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide
                                                                                                                Pei De
                                                                                                                                             Chang Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chang Yi
                                             PREPTIDES DERIVED
FROM THE NON-STRUCTURAL PROTEINS OF
FOOT AND MOUTH DISEASE VIRUS AS
DIAGNOSTIC REAGENTS
                                                                                                                                                                                                                                                                                                                                                       53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEPTIDES DERIVED
FROM THE NON-STRUCTURAL PROTEINS
FOOT AND MOUTH DISEASE VIRUS AS
DIAGNOSTIC REAGENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29,323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1151-4152
                                                                                                                                                                                                                                                                                                                                                    Score 36; DB
Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                   Length 19;
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345 Park

Avenue

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; MOLECULE TYPE: US-08-943-173-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE, CHARACTERISTICS: LENGTH: 58 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
FILING DATE:
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Lin, Maria C.H.
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chen, Ped De
TITLE OF INVENTION: PEPTIDES DERIVED
TITLE OF INVENTION: FROM THE NON-STRUCTURAL PROTEINS
TITLE OF INVENTION: FROM THE NOUTH DISEASE VIRUS AS
                                                                                                                                 ZIF: 10154-0053

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/943,173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 29, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                           STREET: 345 Pa
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                             ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EROKPLKVKAKAPVV 45
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Lin, Maria C.H.
29,323
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212-751-6849
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16
                                                                                                                   US/08/943,173
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Pred. No. 15;
1; Mismatches
                   1151-4152
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MOLECULE TYPE: peptide US-08-943-173-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Guo, Betty
APPLICANT: Hanson, Mark
TITLE OF INVENTION: DbpA AND DbpB COMPOSITIONS ANI
TITLE REFERENCE: 4210.000500
FILE REFERENCE: 4210.000500
CURRENT APPLICATION NUMBER: US/09/117,257
CURRENT FILING DATE: 1998-07-22
EARLIER APPLICATION NUMBER: PCT/US96/17081
EARLIER FILING DATE: 1996-10-22
EARLIER FILING DATE: 1996-10-22
EARLIER FILING DATE: 1996-01-23
EARLIER APPLICATION NUMBER: 08/589,711
EARLIER APPLICATION NUMBER: 08/427,023
EARLIER APPLICATION NUMBER: 08/427,023
EARLIER APPLICATION NUMBER: 08/427,023
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US-09-117-257-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Borrelia afzelii
US-09-117-257-19
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                                                                                                                                                                                                                                                                             US-08-945-476-19
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Best Local Similarity 53.3%;

Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hook, Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver.
SEQ ID NO 19
LENGTH: 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence 19, Application US/09117257
Patent No. 6214355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 212-758-480
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                  Sequence 19, Application US/08945476 Patent No. 6248517
                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 47.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 66
                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
TITLE OF INVENTION: DECORIN BINDING PROTEIN COMPOSITION TITLE OF INVENTION: METHODS OF USE

NUMBER OF SEQUENCES: 27

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION NUMBER: US/08/945,476
                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 ERQKPLKVKAKAPVV 45
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                                                                                                                                                                                                                                                                                                                                                     139 EKTPTTTAEGIITIAKA 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.48;
                                                                                                                                             DECORIN BINDING PROTEIN COMPOSITIONS AND METHODS OF USE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>ب</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 4;
Pred. No. 53;
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FILING DATE:

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APPLICANT: Hook, Magnus
APPLICANT: Guo, Betty
APPLICANT: Hanson, Mark
TITLE OF INVENTION. DbpA AND DbpB COMPOSITIONS AND METHODS OF USE
FILE REFERENCE: 4210.000500
CURRENT APPLICATION NUMBER: US/09/117,257
CURRENT FILING DATE: 1998-07-22
EARLIER APPLICATION NUMBER: PCT/US96/17081
EARLIER FILING DATE: 1996-10-22
EARLIER APPLICATION NUMBER: 08/589,711
EARLIER FILING DATE: 1996-01-22
EARLIER APPLICATION NUMBER: 08/589,711
EARLIER APPLICATION NUMBER: 08/589,711
                                                                                                                                                                                  US-08-458-555-2
                                                                                                                                                                                                                                                      Дb
                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Borrelia afzelii
US-09-117-257-48
                                                                                                                              Sequence 2, Application US/08458555
Patent No. 5840689
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-117-257-48
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                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER FILING DATE: 1995-04-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
                                             APPLICANT: Daniloff, Joanne K
APPLICANT: Meintjes, Elmarie
TITLE OF INVENTION: Method for
TITLE OF INVENTION: Neurons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 19
                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                           3 EKTPLTTAAXAPVVXNA 19
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TOPOLOGY: linb-
)LECTIF
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nes 8; Conserv
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                                                                                                                                                                                                                                               EKTPTTTAEGIITIAKA 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 182
E: John H. Runnels
P. O. Box 2471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09117257
                                                                                                                                                                                                                                                                                                            Conservative
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                                                                     Method for Stimulating the Regrowth of
                                                                                                                                                                                                                                                                                                                             44.48;
47.18;
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Pred. No. 53;

    Mismatches

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                                                                                                                                                                                                                                                                                                          Indels
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RESULT 15
US-07-821-717B-6
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US-08-458-555-2
                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Miller,
APPLICANT: Cunning)
APPLICANT: Lyle, V.
APPLICANT: Finch,
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/07821717B Patent No. 5298239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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ZIP: 70821-24/1
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COMPUTER: PC-DOS/MS-DOS
COMPUTER: PC-DOS/MS-DOS
            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 504 387-322
TELEFAX: 504 346-8049
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                APPLICANT: Finch, Clara N.

TITLE OF INVENTION: MUTATIONS RENDERING PLATELET

TITLE OF INVENTION: GLYCOPROTEIN ID ALPHA LESS REACTIVE
                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE:
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 33451
REFERENCE/DOCKET NUMBER: Att
TELECOMMUNICATION INFORMATION:
TELEPHONE: 504 387-3221
                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Runnels, John H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 29-OCT-1993
 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308 ETTPLTEPEKAPV 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                SOFTWARE:
                                                                                                                                                       COUNTRY:
                                                                                                                                                                         STATE:
                                                                                                                                                                                    CITY: Rochester
                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 8; Conserv
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
                                                                                                                                     14603
                                                                                                                                                                     New York
                                                                                                                                                                                                  Clinton Square, P.O.
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                                                                                                                                                                                                                                                                                                                      Miller, Jonathan L.
Cunningham, David
Lyle, Vicki A.
                                           PatentIn Release #1.0, Version #1.30
                                                                                                                                                     USA
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Linton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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MBER: US/07/821,717B
15-JAN-1992
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61.58;
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Pred. No. 1.1e+02;
Pred. No. 5;
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APTOREMY/ACENT INFORMATION:
ANNE: TIMOH, INFORMATION:
ANNE: TIMOH, INFORMATION:
ANNE: TIMOH, INFORMATION:
TELEPONDOCKET NUMBER: 2084/21
TELECOMMUNICATION INFORMATION:
TELEPONDOCKET NUMBER: 2084/21
TOPOLOGY: 11near
TOPOLOGY: 1
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Title:
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Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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38
3.
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39
39
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Gapop 10.0 , Gapext 0.5
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  GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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## ALIGNMENTS

RESULT 2 A58663 Cotalase (EC 1.11.1.6) [validated] - Proteus mirabilis Cotalase (EC 1.11.1.6) [validated] - Proteus mirabilis Cotales: Proteus mirabilis A; Variety: Strain Pr. peroxide resistant C; Species: Proteus mirabilis A; Variety: Strain Pr. peroxide resistant C; Date: 19-Nov-1997 #sequence_revision 21-Nov-1997 #text_change 15-Sep-2000 C; Date: 19-Nov-1997 #sequence_revision 21-Nov-1997 #text_change 15-Sep-2000 C; Date: 19-Nov-1997 #sequence 11-Nov-1997 #text_change 15-Sep-2000 C; Date: 19-Nov-1997 #sequence 11-Nov-1997 #text_change 15-Sep-2000 C; Date: 19-Nov-1997 #sequence 11-Nov-1997 #text_change 15-Sep-2000 C; Date: 14-59-72, 1995 A; Title: Complete amino acid sequence of Proteus mirabilis PR catalase. Occurrence of A; A; Title: Complete amino acid sequence of Proteus mirabilis PR catalase. Occurrence of A; A; Title: Complete amino acid sequence of Proteus mirabilis PR catalase. Occurrence of A; A; Title: Complete amino acid sequence of Proteus mirabilis PR catalase. Occurrence of A; A; Title: Complete amino acid sequence of Proteus mirabilis PR catalase. Occurrence of A; A; Title: Complete amino acid sequence of Proteus mirabilis PR catalase. Occurrence of A; A; Title: Complete amino acid sequence of Proteus mirabilis PR catalase. Occurrence of A; A; Title: Complete amino acid sequence of Proteus mirabilis PR catalase. Occurrence of A; A; Title: Complete amino acid sequence of Proteus mirabilis PR catalase. Occurrence of A; A; Cotalase. A; Title: Complete amino acid sequence of Proteus mirabilis PR catalase. Occurrence of A; Title: Complete amino acid sequence of Proteus mirabilis PR catalase. Occurrence of A; Title: Complete amino acid sequence of Proteus mirabilis PR catalase. Occurrence of A; Title: Complete amino acid sequence of Proteus mirabilis PR catalase. Occurrence of A; Title: Complete amino acid sequence of Proteus mirabilis PR catalase. Occurrence of A; Title: Complete amino acid sequence of Proteus mirabilis PR catalase. Occurrence of A; Title: Complete amino acid sequence of Proteus mi	Query Match 77.8%; Score 63; DB 2; Length 482; Best Local Similarity 82.4%; pred. No. 0.0032; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0; Qy 2 EEKTPLTTAAXAPVVXN 18	A;Status; preliminary A;Molecule type: DNA A;Residues: 1-482 <sto> A;Cross-references: GB:AE004841; GB:AE004091; NID:g9950451; PIDN:AAG07624.1; GSPDB:GN A;Cross-references: GB:AE004841; GB:AE004091; NID:g9950451; PIDN:AAG07624.1; GSPDB:GN A;Experimental source: Strain PAO1 C;Genetics: C;Genetics: A;Gene: katA; PA4236 C;Superfamily: catalase</sto>	RESULT 1  B83113  catalase PA4236 [imported] - Pseudomonas aeruginosa (strain PAO1)  catalase PA4236 [imported] - Pseudomonas aeruginosa (strain PAO1)  c;Species: Pseudomonas aeruginosa  c;Species: Pseudomonas aeruginosa  c;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000  c;Accession: B83113  R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;  adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L  adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L  adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L  adman, S.; Yuan, Y.; Olson, M.V.  Nature 406, 959-964, 2000  A; Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa  A; Accession: B83113

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* RESULT
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                                                                                                                                   Query Match
Best Local Similarity
Matches 9; Conserv
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A;Contents: annotation; X-ray crystallography, 2.2 angstroms
C;Complex: homotetramer
C;Function:
A;Description: catalyzes the conversion of two of molecules of hydrogen peroxide to two A;Note: this enzyme has a tightly bound NADPH cofactor
C;Superfamily: catalase
C;Superfamily: catalase
C;Superfamily: catalase
C;Superfamily: catalase
F;33/Modified site: methionine sulfone (Met) #status experimental
F;33/Binding site: heme iron (Tyr) (axial ligand) #status experimental
                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-262 <LAT>
A;Cross-references: EMBL:AF078784; PIDN:AAC26925.1; GSPDB:GN00021; CESP:H34I24.2
A;Experimental source: strain Bristol N2; clone H34I24
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Latreille, P.; Wamsley, P.; O'Brien, D. submitted to the EMBL Data Library, July 1998 A;Description: The sequence of C. elegans cos
                                                                                                                                                                                                                                                                            A; Map position:
A; Note: intron p
                                                                                                                                                                                                                                                                                                                        A; Gene: CESP: H34I24.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: Z21340
A; Accession: T33408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: Caenorhabditis elegans
Date: 29-Oct-1999 #sequence_revision
C:Accession: T33408
R:Latreille, P.; Wamsley, P.; O'Brien,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translated from
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R;Gouet, P; Jouve, H;M.; Hajdu, J.
submitted to the Brookhaven Protein Data Bank, June 1996
A:Reference number: A67900; PDB:2CAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Contents: annotation; x-ray crystallography, A; Note: compound II, dithiothreitol reduced con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ypothetical protein H34I24.2 · Caenorhabditis elegans (fragment)
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Matches 12
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                                                            190 KTPLTSGSSARVINNA 205
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les 12; Conserv
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                                                                                                                                                  Conservative
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75.0%;
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Pred. No. 0.17;
                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cosmid H34I24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      compound
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                                                                                                                                                  4;
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                                                                                                                                                                                           Length 262;
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                                                                                                                                             Indels
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A; Start codon: C; Superfamily:
                                                C; Genetics:
                                                            A:Residues: 1-483 <FAC>
A;Cross-references: EMBL:X74791;
A;Note: the source is designated
                                                                                                                     A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                   C;Accession: S37055
R;Facey, S.; van Pee, K.H.; Vining, submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                  catalase (EC 1.11.1.6) alpha-2 chain -
C:Species: Streptomyces violaceus
C:Date: 10-Dec-1993 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
3; Conserve
                                                                                                                                                                   A; Accession: S37055
                                                                                                                                                                                    A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-427 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M89911; NID:g153436; PIDN:AAA26811.1; C;Superfamily: Escherichia coli ribosomal protein L12 C;Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: AT4g36970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:NC_001268; NID:g7270646; PIDN:CAB80363.1; GSPDB:GN00140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;anonymous, The European Union Arabidopsis Genome Nature 402, 769-777, 1999
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A;Accession: JC1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Parra, F.; Blanco, G.; Alonso, J.M.M.; Balbin, M.; Mendez, Gene 118, 127-129, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A85001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Sequence and analysis of chromosome 4 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F85436
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A; Residues: 1-128 <P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ribosomal protein L7/L12 - Streptomyces antibioticus C;Species: Streptomyces antibioticus C;Species: Streptomyces antibioticus C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999 C;Accession: JC1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JC1273
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Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                           208 EEKAEMTTAMOSPVV 222
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les 10; Conserv
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                                                                                                  1-483 <FAC>
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                           GTG
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                                                                                                                                                                                      S37055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.3%;
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66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUID:20083488
                                                            NID:g397888; PIDN:CAA52796.1; PID:g581780 as Streptomyces venezuelae

    Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB 2;
Pred. No. 0.98;
                                                                                                                                                                                                   L.C.
August 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                            26-May-1995 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                    Streptomyces violaceus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
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Зþ

catalase

Page

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C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase F;54,93,127/Active site: His, Ser, Asn #status predicted F;337/Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               catalase (EC 1.11.1.6) - Streptomyces coelicolor (fragments) C;Species: Streptomyces coelicolor C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change C;Accession: A44639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
A44639
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T08462

C:Species: Arabidopsis thaliana (mouse-ear ceress)

C:Species: Arabidopsis thaliana (mouse-ear ceress)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999

C:Accession: T08462

R:Quetier, F: Purnelle, B.: Boutry, M.; Goffeau, A.; Salanoubat, M.; Mewes, submitted to the Protein Sequence Database, May 1999

A:Reference number: Z16420

A:Accession: T08462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: catalase
C; Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 1-105 <WAL>C; Superfamily: catalase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Walker, G.
submitted to the Protein
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hypothetical protein T25B15.140 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
                                                   RESULT
T46107
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Accession: A44639
Status: preliminary
Molecula + ******
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Best Local
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                                                                                                                                                                                                                                                                        A; Map
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Best Local S
Matches 9
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                                                                                                                                                                                                                                                                                                        Genetics:
                                                                                                                                                                                      Query Match
Best Local Similarity 50.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                          position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y match 51.9%;
Local Similarity 69.2%;
hes 9; Conservative
                                                                                                                         291
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                                                                                                                                                                                                                                                                                        ATSP: F2206.250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLTTVAGAPVPDN: 19
                                                                                                                       EEKTPVEKKTGVPVVKKA 308
                                                                                                                                         EEKTPLTTAAXAPVVXNA 19
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9; Conserv
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pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Pred. No. 2.6;
                                                                                                                                                                                                          Score 42;
Pred. No.
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C;Accession: T46107
R;Alcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, R.; submitted to the Protein Sequence Database, January 20 A;Reference number: Z23021
A;Accession: T46107
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A; Molecule type: DNA
A; Residues: 1-436 <ALC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 3
A; Introns: 418/1
A; Note: T25B15.140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: T50779
R;Himelblau, E; Mira, H.; Lin, S.J.; Culotta, V.C.; Penarrubia, Piant Physiol. 117, 1227-1234, 1998
A;Title: Identification of a functional homolog of the yeast copp A;Reference number: 224450; MUID:9701579
A;Accession: T50779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  copper chaperone homolog CCH [imported] - rice
C;Species: Oryza sativa (rice)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T50779
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                                                                                                                                                                        R;DeShazer, D.; Wood, G.E.; Friedman, R.L.
Mol. Microbiol. 14, 123-130, 1994
A;Title: Molecular characterization of catalase from Bor
A;Reference number: S60757; MUID:95131725
A;Accession: S60757
A;Status: preliminary; nucleic acid sequence not shown;
A;Status: preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                                 catalase (EC 1.11.1.6) - Bordetella pertussis
C;Species: Bordetella pertussis
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change
C;Accession: S60757
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S60757
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C;Superfamily: catalase C;Keywords: chromoprotein; heme; iron; metalloprotein; oz;Keywords: chromoprotein; heme; iron; metalloprotein; c;F,796,130/Active site: His, Ser, Asn #status predicted F;340/Binding site: heme iron (Tyr) (axial ligand) #status
                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-482 <DES>
                                                                       A; Gene: catA
                                                                                        C; Genetics:
                                                                                                      A; Note: the nucleotide sequence was submitted
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RESULT
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DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy.
A;Reference number: A72450; MUID:99310339
                                                                                                                                                                                          A; Gene:
                                                                                                                                                                                                            A;Cross-references: DDBJ:AP000064; NID:g5105945; PIDN:BAA81416.1; PID:d1045202; PID:g510A;Experimental source: strain Kl
                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-252 <KAW>
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H72469
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awa, H.; Takamiya, M.; Masuda, S.; Funahashi,
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A;Residues: 1-171 <WIL>
A;Cross references: EMBL:Z82273; PIDN:CAB54978.1; GSPDB:GN00022; CESD:F56F12.1
                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein APE2401 -
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ubmitted to the EMBL Data Library, October 1999
Reference number: Z21039
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Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
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i, T.; Tanaka, T.; Kudoh, Y.; Yamazaki,
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A;Cross-references: FlyBase:FBgn0015168
A;Mobile element: retrotransposon ninja
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                                                                                                                                                                                                                                                                       R:Ogura, K.; Takechi, S.; Nakayama, T.; Yamamoto, M. Genes Genet. Syst. 71, 1-8, 1996
Genes Genet. Syst. 71, 1-8, 1996
A:Title: Molecular structure of the transposable element ninja in Drosophila simulans
A:Reference number: Z21057; MUID:96252483
A:Accession: T31674
                                                                                                                                                                                                                                                                                                                                                                   C:Species: Drosophila simulans
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change
C:Accession: T31674
                                                                                                                                                                                A;Cross-references: EMBL:D83207; NID:d1068446; PID:d1020552; PIDN:BAA19771.1
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A:Map position: 2R 60C5-C8
C;Keywords: G protein-coupled receptor;
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A;Residues: 81-154 'T',156-198,'N',200-215,'G',217-227,229-330,'P',332-426,'YATPVTIET
A;Cross-references: GB:M27495
                                                             Query Match
Best Local
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A; Residues: 1-788 < ONA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Onai, T.; FitzGerald, M.G.; Arakawa, S.; FEBS Lett. 255, 219-225, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            muscarinic acetylcholine receptor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 15-Oct-1999
C:Accession: S05661; A36191
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EKTPLTTAAXAPVVXNA 19
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PRINTS; PR00067; CATALASE, 1.
ProDom; PD000510; Catalase; 1.
PROSITE; PS00434; CATALASE, 1.
PROSITE; PS00438; CATALASE, 1.
                                                                                                                                                                      MEDLINE-SS311317; PubMed=7791219;
Gouet P., Jouve H.-M., Dideberg O.;
"Crystal structure of Proteus mirabilis PR catalase with bound NADPH.";
J. Mol. Biol. 249;933-954(1995).
-!- FUNCTION: DECÓMPOSES HYDROGEN PEROXIDE IN WATER AND TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN COPTACTOR: HEME GROUP AND NADP.
-!- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
                PRINTS; PR00067; CATALASE.
ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
                                                                     PDB; 2CAE; 08-DEC 96.
PDB; 2CAF; 07-DEC 96.
PDB; 2CAF; 07-DEC 96.
PDB; 2CAH; 11-JAN-97.
InterPro; IPR002226; Catalase.
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ACT_SITE 55
ACT_SITE 128
BINDING 338
SEQUENCE 482 AA;
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CATA_PROMI
P42321;
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-i- MASS SPECTROMETRY: MW=55643; MW_ERR=5; METHOD-ELECTROSPRAY.
-i- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                -!- COFACTOR: HEME GROUP AN
                                                                                                                                                                                                                                                                                                                             MEDLINE=95305957; PubMed=7786407;
Buzy A., Bracchi V., Sterjiades R., Chroboczek J.,
Gagnon J., Jouve H.-M., Hudry-Clergeon G.;
"Complete amino acid sequence of Proteus mirabilis
Occurrence of a methionine sulfone in the close pro-
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01-NOV-1995
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nes 14; Conserv
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      Peroxidase; Iron; Heme;
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of Proteus mirabilis PR catalase with
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PROXIMAL HEME LIGAND (BY SIMILARITY).
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Pfam; PF00542; Ribosomal_L12; 1.
ProDom; PD001326; Ribosomal_L12; 1.
Ribosomal protein.
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PIR; JC1273; JC1273.
HSSP; P02392; ICTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parra F., Blanco G., Alonso J.M., Balbin M., Mendez C., Salas J.P.
"Cloning and sequence of a gene encoding the L7/L12 ribosomal pro-
equivalent of Streptomyces antibioticus.";

Gene 118:127-129(1992).

I. FUNCTION: SEEMS TO BE THE BINDING SITE FOR SEVERAL OF THE FAC-
INVOLVED IN PROTEIN SYNTHESIS AND APPEARS TO BE ESSENTIAL FOR
ACCURATE TRANSLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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01-DEC-1992
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ADC25F3CB41F5C50 CRC64;
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Best Local
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Facey S., Gross F., Vining L.C., Yang K., van Pee K.-H.;
Facey S., Gross F., Vining L.C., Yang K., van Pee K.-H.;
Facey S., Gross F., Vining L.C., Yang K., van Pee K.-H.;
Facey S., Gross F., Vining L.C., Yang K., van Pee K.-H.;
Facey S., Gross F., Vining L.C., Yang K., van Pee K.-H.;
Facey S., Gross F., Vining K., Van Pee K.-H.;
Facey S., Van Fee K.-H.;
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Bacterla; Firmicutes; Actinobacterla; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCA.
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01-OCT-1996 (Rel. 34, Last annotation update)
BROMOPEROXIDASE-CATALASE (EC 1.11.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by
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NCBI_TaxID=1936;
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ACT_SITE
BINDING
SEQUENCE
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PIR; S37055; S37055.
HSSP; P42321; 2CAH.
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STRAIN-ATCC 10712 / ISP5230;
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proSiTE; PS00437; CATALASE_1; 1.
proSiTE; PS00438; CATALASE_2; 1.
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                                                                                                                                                                                                                                                                      O1-FEB-1996 (Rel. 33, Created)
O1-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CATALASE (EC 1.11.1.6).
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  Bordetella pertussis.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                   P48062;
                                                                                                                                                           NCBI_TaxID=520;
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                                                                                                                                                                                                                                                     KATA
                                                                                          STRAIN-BP504;
                                                                                                                  SEQUENCE FROM N.A.
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BY SIMILARITY.
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BY SIMILARITY (BY SIMILARITY).
PROXIMAL HEME LIGAND (BY SIMILARITY).
W; B58CF8230B8A2F55 CRC64;
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ACM1_DROME
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ACT_SITE 57
ACT_SITE 130
BINDING 340
SEQUENCE 482 A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
MUSCARINIC ACETYLCHOLINE RECEPTOR DM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1;
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                        MEDLINE-90005981; PubMed-2507354;
Onai T., Fitzgerald M.G., Arakawa S., Gocayne J.D., Urquhart D.A.,
Hall L.M., Fraser C.M., McCombie W.R., Venter J.C.;
"Cloning, sequence analysis and chromosome localization of a
Drosophila muscarinic acetylcholine receptor.";
FEBS Lett. 255:219-225(1989).
-i- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shapiro R.A., Wakimoto B.T., Subers E.M., Nathanson N.M. "Characterization and functional expression in mammalian genomic and cDNA clones encoding a Drosophila muscarinic acetylcholine receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ephydroidea; Dro
NCBI_TaxID=7227;
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Eukaryota; Metazoa; Arthropoda; Tra
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SIMILARITY: BELONGS TO THE CATALASE FAMILY.
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PS00438; CATALASE_2; 1.
uctase; Peroxidase; Iron;
57 57 BY SI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18
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BY SIMILARITY.
BY SIMILARITY.
PROXIMAL HEME LIGAND (BY SIMILARITY).
7CB73E08975C219F CRC64;
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Pred.
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  It is produced through a collaboration -
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RESULT 7
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Best Local
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DOWALN 1 26
TRANSMEM 27 49
DOWALN 50 60
TRANSMEM 61 81
                                                                                                                                                                                                                                                                                  CARBOHYD
CARROHYD
CONFLICT
         P78567;
01-NOV-1997
                                       H2B_AGABI
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Pfam; PRO0001; 7tm_1; 1.
Pfam; PRO0001; 7tm_1; 1.
PRINTS; PRO0237; GPCRRHODOPSN.
PRINTS; PRO0243; MUSCARINICR.
PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G-PROTEIN_RECEP_F1_2; 1
PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1
PS50262; G-PROTEIN_RECEP_F1_2; 1
PS50262; G-PROTEIN_RECEP_F1_2; 1
PS502625; G-PROTEIN_RECEP_F1_2; 1
PS502625; G-PROTEIN_RECEP_F1_2; 1
PS502625; G-PROTEIN_RECEP_F1_2; 1
PS502625; G-PROTEIN_RECEP_F1_2; 1

                                                                                                                   538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase; FBgn0000037; mAcR-60C.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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EMBL; M23412; AAA28676.1; ALT_INIT.
PIR; A36191; A36191
PIR; S05661; S05661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute.
                                                                                                                                             3 EKTPLTTAAXAPVVXNA 19
                                                                                                               EDGPTTTAAAAPLASAA 554
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                           Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCR_0024; -.
         (Rel. 35, Created)
                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209
635
657
673
                                      STANDARD;
                                                                                                                                                                                                                                                    AA;
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1136
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362
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451
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606
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686
688
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722
78237
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                                                                                                                                                                                      49.48;
52.98;
                                                                                                                                                                                                                                                    MW;
                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC...

T -> A (IN REF. 2).

N -> S (IN REF. 2).

G -> R (IN REF. 2).

A -> AA (IN REF. 2).

P -> G (IN REF. 2).

MISSING (IN REF. 2).

G -> A (IN REF. 2).

T -> A (IN REF. 2).

C -> VG (IN REF. 2).

P -> AR (IN REF. 2).
                                                                                                                                                                         1;
                                                                                                                                                                      Score 40; DB : Pred. No. 26; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (POTENTIAL),
CYTOPLASMIC (POTENTIAL)
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CYTOPLASMIC (I
4 (POTENTIAL)
                                                                                                                                                                                                                                                                               VLI ->
                                                                                                                                                                                                                                                            EGMVRGVYN -> DFYAASTIR (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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                                                                                                                                                                                                                                                  FB35417CB2202A61 CRC64;
                                                                                                                                                                                                                                                                  > CXS (IN REF. 1).
> C (IN REF. 2).
RGVYN -
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> G (IN REF. 2).
SING (IN REF. 2).
SING (IN REF. 2).
> A (IN REF. 2).
> VG (IN REF. 2).
> AR (IN REF. 2).
                                    143
                                    ΑA
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DMPC_PSESP
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Best Local S
Matches 8
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DMPC_PSESP
P19059;
01-NOV-1990
Nordlund I., Shingler V.;

Nordlund I., Shingler V.;

"Nucleotide sequences of the meta-cleavage pathway enzymes hydroxymuconic semialdehyde dehydrogenase and 2-hydroxymucoc semialdehyde hydrolase from Pseudomonas CF600.";

Biochim. Biophys. Acta 1049:227-230(1990).

-!- FUNCTION: 2-HYDROXYMUCONIC ACID SEMIALDEHYDE CAN BE CON-
                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=90304229; PubMed=2194577;
                                                                                                                                                                                                                                           Pseudomonas sp. Plasmid pVI150.
                                                                                                                                                                                                                                                                                                       01-NOV-1990 (Rel.
15-JUL-1998 (Rel.
2-HYDROXYMUCONIC S
                                                                                                                                                                                                                                                                                                                            01-NOV-1990
15-JUL-1998
                                                                                                                                                                                                                       Bacteria; Proteobacteria
                                                                                                                                                                                                    NCBI_TaxID=306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chromosomal protein; Nucleosome SEQUENCE 143 AA; 15165 MW; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00427; H2B; 1.
PROSITE; PS00357; HISTONE_H2B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000497; Histone_H2B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00621; HISTONEH2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00125; histone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000558; Histone_H2B.
InterPro; IPR000166; Histone_core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X94188; CAA63898.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      assignment to chromosomes. Appl. Environ. Microbiol. -! - SUBUNIT: THE NUCLEOSOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sonnenberg A.S.M., de Groot P.W.J., Schaap P.J., Baars J.J.P., Visser J., van Griensven L.J.L.D.;
"Isolation of expressed sequence tags of Agaricus bisporus and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97111990; PubMed=8953726;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=5341;
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Eukaryota; Fungi;
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30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HISTONE H2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 KTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE HISTONE H2B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. Environ. Microbiol. 62:4542-4547(1996).
SUBUNIT: THE NUCLECSOME IS AN OCTAMER CONTAINING
H2A, H2B, H3, AND H4; WHICH WRAP APPROXIMATELY 14
SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KAPASTASKAPVKSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 50.8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                              (strain CF600).
                                                                                                                                                                                                                                                                                              . 16, Created)
. 16, Last sequence update)
. 36, Last annotation update
SEMIALDEHYDE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Common mushroom).

Basidiomycota; Hymenomycetes; Homobasidiomycetes; caceae; Agaricus.
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39,
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50.0%;
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Last annotation updat
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Pred. No. 7.4;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          core; Nuclear protein; 69640102E31F4B56 CRC64;
                                                                                                                                                                                                                                                                                                                          update)
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7.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 143;
                                                                                                                                                                                                                                                                                              1.2.1.-) (HMSD)
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146 BP OF DNA.
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SEMIALDEHYDE CAN BE CONVERTED TO

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RESULT 9
YB64_YM
1D YB64_Y
1D YB64_Y
1D YB64_Y
1D YB64_Y
1D YB64_Y
1D YB64_Y
1D 1-OCT
1D 1-OC
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Best Local S
Matches 9
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THREE SEQUENTIAL ENZYMES, THE FIRST OF WHICH IS HMSD.
THREE SEQUENTIAL ENZYMES, THE FIRST OF WHICH IS HMSD.
THEREALY HETA-CLEAVAGE PATHWAY FOR THE DEGRADATION OF PHENOLS, CRESOLS AND CATECHOL. PHENOL METABOLISM.
CRESOLS AND CATECHOL. PHENOL METABOLISM.
CRESOLS AND CATECHOL. PHENOL METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way entities and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPKUVACO-, PROMOTOR CYS; 1.
Pfam; PF00171; aldedh; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_GUU; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GUB; Oxidoreductase; NAD; Plasmid. Aromatic hydrocarbons catabolism; Oxidoreductase; NAD; Plasmid. Aromatic hydrocarbons catabolism; Oxidoreductase; NAD; Plasmid. Aromatic hydrocarbons catabolism; Oxidoreductase; NAD; Plasmid. Aromatic hydrocarbons about 1.
PROSITE 254 254 BY SIMILARITY.
ACT_SITE 258 288 288 BY SIMILARITY.

258 288 288 C1682 MW; F906FCA64185AA68 CRC64;
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PIR; S10772; S10772.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 57.2 KDA PROTEIN IN MET8-HPC2 INTERGENIC REGION
YBR214W OR YBR1501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YB64_YEAST
P38314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungl; Ascomycota; Saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 EETPLTTALLGEVMQAA 197
                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                      Dubols E., el Bakkoury M., Glansdorff N., Messenguy F., Pierard Scherens B., Vierendeels F.; Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases. Submitted (AUG-1994) TO TEMPLOSEC AND S.POMBE SDS23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 114-527 FROM N.A.
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9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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pred. No.
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Best Local S
Matches 8
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Pfam; PF00571; CBS; 3

SMART; SM00116; CBS; 2.

Hypothetical protein; Repeat; CB; 251

DOMAIN 283 335

SEQUENCE 527 AA; 57187 MW; 1
RESULT 11
GYRB_MYXXA
ID GYRB_M
AC 033367
DT 15-DEC
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                                                                                                                                                                                                                                                                      Query Match
Best Local S
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$GD; $0000418; $D$2
InterPro; IPR000644
                                                                                                                                                                                                                                                        Matches
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13-AUG-1987
13-AUG-1987
01-MAY-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Influenza B virus (strain B/Lee/40).
Viruses; ssRNA negative-strand viruses; Orthomyxovirldae;
Influenza virus A and B group; Influenza B virus.
NCBI_TaxID-11535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is on no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE-84174071; PubMed-6324462;

MEDLINE-84174071; PubMed-6324462;

Briedis D.J., Tobin M.;

Briedis D.J., Tobin M.;

Influenza B virus genome: complete nucleotide sequence of influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 virus genome RNA segment 5 encoding the influenza B/lee/40 
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                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; K01395; AAA43689.1; -.
InterPro; IPR002141; F1u_NP.
Pfam; PF00596; F1u_NP; 1.
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                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
GYRB_MYXXA STANDARD;
033367;
15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                                           Nucleoprotein
                                                                                                                                                            19 EELTPGTSGATRPIIKPA
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8; Conserv
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8; Conservative
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(Rel.
(Rel.
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                                                                                                                                                                                                                                                                                                                                                                            560 AA;
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05, Last sequence up
22, Last annotation
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                                                                                                                                                                                                                                                                                                                                                                               61770 MW;
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Pred. No.
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                                                                                                                                                                                                                                                                                        Score 39; DB pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                 74C4FEAF9E75A695 CRC64;
                                                                                                                                                                                                                                                                         Mismatches
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RESULT 12
GBP_PSE_P
ID GBP_P
AC 02791
DT 15-JU
DT 15-JU
DT 15-JU
DT GROWT
OS Pseud
OC Ptery
OC Noctu
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Best Local
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InterPro; IPRO01241; DNA_topoisoII.
InterPro; IPRO01294; HATPase_C.
InterPro; IPRO02594; HATPase_C.
InterPro; IPRO02936; Toprim.
InterPro; IPRO02936; Toprim; 1.
InterPro; IPRO02936; DNA_topoisoII; 1.
InterPro; IPRO0159; DNAGYRASEB.
IPRODom; PD000616; DNA_topoisoII; 1.
IPRODom; PD14963; DNA_GYRASEB.
IPRODom; PD14963; DNA_GYRASEB.
IPRODom; SM0483; DNA_GYRASEB.
IPR
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-JUL-19
                                                                                                                                                                                                                                                                                                          GBP_PSESE
Q27913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Topoisomerase;
SEQUENCE 815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=34;
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                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isomerase; ATP-binding.
AA; 89636 MW; 3862685FBB805B32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     teobacteria; delta subdivision; Myxobacteria;
Cystobacterineae; Myxococcaceae; Myxococcus;
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66.78;
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Pred. No. 44;
                                                                                                                                                                                                                                                                                                                    PRT;
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RESULT 13
PLL_CORPS
ID PLL_CORPS
AC P2062
DT 01-FE
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DE PHOSP
GN PLD
OC Bacte
OC Actin
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OX NCBI_
RN [1]
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P20626; Q59314; Create
01-FEB-1991 (Rel. 17, Create
01-FEB-1991 (Rel. 17, Last :
01-NOV-1997 (Rel. 35, Last :
PHOSPHOLIPASE D PRECURSOR ()
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Bacteria; Firmiculus; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacterium.

COrynebacterium.

NCBI_TaxID=1719;

[1]
                                                       Corynebacterium pseudotuberculosis
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DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02425; GBP_PSP;
                                                                                                                                                                                                                                                                                                                                                                                      PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
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Kawano K., Hikichi K., Nitta K.;
"Solution structure of an insect growth factor, growth-blocking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99107831; PubMed=9890941;
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MEDLINE=98316655; PubMed=9654083;
Hayakawa Y. Noguchi H.;
"Growth-blocking peptide expressed in the cloning and functional chracterization."
Eur. J. Biochem. 253:810-816(1998).
                                                                                                                                                                                                                                            2 EEKTP--LTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE BY NMR OF 121-143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayakawa Y., Ohnishi A., Yamanaka A., Iz
"Molecular cloning and characterization
peptide, growth-blocking peptide.";
FEBS Lett. 376:185-189(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96105377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 274:1887-1890(1999).
FUNCTION: BIOGENIC PEPTIDE THAT PREVENTS, IN LEPIDOPTERAN, THE ONGET OF METAMORPHOSIS FROM LARVA TO PUPA. THIS GROWTH-BLOCKING PEPTIDE HAS REPRESSIVE ACTIVITY AGTONST JUPENILE HORMONE ESTERASE.
SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                               ; AB012294; BAA32793.1; -
1BQF; 09-DEC-98.

**Pro; IPR003463; GBP_PSP.
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127
143
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139
15256
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Last annotation update)
(RSOR (EC 3.1.4.4) (PLD)
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50.0%;
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                          GROWTH-BLOCKING PEPTIDE
                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
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                                                                                                                                                                                                                                                                                           1; Length 143,
                                                                        (CHOLINE PHOSPHATASE)
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MCNamara P.J., Bradley G.A., Songer J.G.;
"Targeted mutagenesis of the phospholipase D gene results decreased virulence of Corynebacterium pseudotuberculosis. Mol. Microbiol. 12:921-930(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MCNamara P.J., Cuevas W.A., Songer J.G.; "Toxic phospholipases D of Corynebacterium ulcerans and Arcanobacterium haemolyticum: homology."; gene 156:113-118(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BIOVAR OVIS / ISOLATE WHETTEN 1;
MEDLINE-90093451: Pubmed-2403529;
Songer J.G., Libby S.J., Tandolo J.J., Cuevas W.A.;
"Cloning and expression of the phospholipase D gene from Corynebacterium pseudotuberculosis in Escherichia coli.";
Infect. Immun. 58:131-136(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 25-47.

MEDLINE=90170833; PubMed=2407718;

MEDGISON A.L.M., Bird P., Nisbet I.T.;

MICHORITY, nucleotide sequence, and expression the phospholipase D gene from Corynebacterium J. Bacteriol. 172:1256-1261(1990).
                                                                                                                                                                              VARIANT
VARIANT
VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND HEMOLYTIC ACTIVITY: A PHOSPHATIDYLCHOLINE + H(2)0 -
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                                                                                                                        SEQUENCE
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FUNCTION: VIRULENCE FACTOR AFFECTING
SURVIVAL WITHIN THE HOST. HAS MAGNES!
                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: TO OTHER CORYNEBACTERIUM PHOSPHOLIPASES
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 PVGNAAAAPVVIIN 30
                          PLTTAAXAPVVXN
                                                    8; Conservative
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POTENTIAL.

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F -> L (IN BIOVAR EQUI / IS

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N -> D (IN BIOVAR EQUI / IS

I -> M (IN BIOVAR EQUI / IS

A -> P (IN BIOVAR EQUI / IS

M; D3B1334E6FC99875 CRC64;
                                                                   Score 38;
Pred. No.
                                                                                                                                                                                                                                                                Magnesium; Virulence;
                                                         Mismatches
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                                                                      DB
24;
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                                                                                  1;
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pseudotuberculosis.";
                                                                                Length 307
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ENT SPHINGOMYELINASE
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RESULT 14 CATA_PSEPU

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Q59714;
30-MAY-2000
30-MAY-2000
30-MAY-2000
                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence up 20-AUG-2001 (Rel. 40, Last annotation ELONGATION FACTOR G 1 (EF-G 1).
FUSA OR FUSA-2 OR TP0767
Treponems
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Kim Y.C., Miller (
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proSITE; pS00437; CATALASE_1; 1.
proSITE; pS00438; CATALASE_2; 1.
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                            Treponema pallidum.
Bacteria; Spirochaetales;
CBI_TaxID=160;
                                                                                                                     EFG1_TRI
083748;
                                                                                                                                                                                                                                                                                                                                    Oxidoreductase;
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Pfam; PF00199; catalase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fidentification of adjacent genes encoding bacterioferritin from the plant-beneficial
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STRAIN-NICHOLS;
         SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN CAPALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
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                                                                                                                                TREPA
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MW; EFE3CBDE67778571 CRC64;
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Search completed: February 28, 2002, 11:39:52 Job time: 308 sec
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Matches 9; Conservative
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PROSITE; PS00301; EFACTOR GTP; 1.

Elongation factor; Protein biosynthesis; GTP-binding;

Multigene family; Complete proteome.

NP_BIND 15 22 GTP (BY SIMILARITY).

NP_BIND 82 86 GTP (BY SIMILARITY).

NP_BIND 136 139 GTP (BY SIMILARITY).

NP_BIND 136 139 GTP (BY SIMILARITY).

SEQUENCE 695 AA; 76831 MW; 46529989BFE97E4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of Treponema pallidum, the syphilis spirochete.";
Science 281:375-388(1998).
-i- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLOCATION OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE RIBOSOME.
-i- SUBCELIULAR LOCATION: CYTOPLASMIC.
-i- SUBCELIULAR LOCATION: CYTOPLASMIC.
-i- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.

EF-G/EF-2 SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
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InterPro; IPR000795; GTP_EFTU.
Pfam; PF00679; EFG_C; 1.
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O9u4y3 ceratitis c
O9y984 aeropyrum p
O9a4b0 caulobacter
O9rd97 streptomyce
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Q9ai19 escherichia
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## ALIGNMENTS

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01-JUN-2001 (TrEMBLrel. 17, La
01-JUN-2001 (TrEMBLrel. 17, La
HYPOTHETICAL PROTEIN H34124.2.
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis
NCBI_TaxID=6239;
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Latreille P., Wamsley P., O'Brien D.;
"The sequence of C. elegans cosmid H34124.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: IPR002226; Catalase.
Pfam; PF00199; Catalase; 1.
PRINTS: PR00067; CATALASE.
ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE.1; 1.
PROSITE; PS00438; CATALASE.2; 1.
Heme; Hydrogen peroxide; Iron; Oxi
SEQUENCE 484 AA; 54961 MW; DDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000
01-MAY-2000
01-JUN-2001
                                            Lalioui L., Le Bouguenec C.C.;
"afa-8 Gene cluster is carried
the tRNA(Phe) of human and bov
                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (Trembirel.
01-JUN-2001 (Trembirel.
01-JUN-2001 (Trembirel.
HYPOTHETICAL 34.4 KDA PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Host-Range Vector: Isolation of Catalase-Deficient Mutants of Actinobacillus actinomycetemcomitans.";
J. Bacteriol. 181:7298-7307(1999).
-i- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGAN SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20042351; PubMed=10572134;
Thomson V.J., Bhattacharjee M.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Actinobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 actinomycetemcomitans)
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                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9AI19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEROXIDE (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: 2 H(2)O(2) =
EMBL; AF162654; AAF17882.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Figurski D.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=714;
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                                                                                                                               MEDLINE=21101044; PubMed=11159989;
                                                                                                                                                                                                                                        NCBI_TaxID=562;
                                                                                                                                                                                                                                                                   Escherichia.
                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                        Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9AI19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P42321;
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1 (TrEMBLIEL 17, Las
1 (TrEMBLIEL 17, Las
1 (TrEMBLIEL 17, Las
AL 34.4 KDA PROTEIN.
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69:937-948(2001).
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                                                                                                                                                                                                                                                                                            gamma subdivision; Enterobacteriaceae;
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                                                 bovine
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subdivision; Pasteurellaceae;
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                                               a pathogenicity island pathogenic Escherichia
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  RESULT
P77924
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023188
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Matches
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Best Local S
Matches
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01-MAY-1999 (TrEMBLrel. 10, La
01-OCT-2000 (TrEMBLrel. 15, La
HYPOTHETICAL 46.8 KDA PROTEIN.
C7A10.390 OR AT4G36970.
Nurk A., Peters M.;
Submitted (SEP-1996) t
-i- FUNCTION: OCCURS I
SERVES TO PROTECT
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Hypothetical protein.
SEQUENCE 314 AA; 34415 M
                                                                                               NCBI_TaxID=294;
                                                                                                                                         Plasmid
                                                                                                                                                      Pseudomonas fluorescens
                                                                                                                                                                                  CATALASE
                                                                                                                                                                                               01-JUN-2001
                                                                                                                                                                                                            01-FEB-1997
01-FEB-1997
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Submitted (MAR-2000) to the
EMBL; 299707; CAB16794.1; -.
EMBL; AL161590; CAB80363.1;
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Chalwatzis N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
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01-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             023188
                                                         STRAIN=CB36;
                                                                      SEQUENCE FROM N.A
                                                                                                               Pseudomonas
                                                                                                                            Bacteria;
                                                                                                                                                                                                                                                    P77924
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                                                                                                                                                                                                                                                                                                                                                EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                        EEKAEMTTAMQSPVV
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9; Conservative
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8; Conser
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                                                                                                                           Proteobacteria;
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427 AA; 40
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47.1%;
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 to the EMBL/GenBank/DDBJ databases.
IN ALMOST ALL AEROBICALLY RESPIRING
I CELLS FROM THE TOXIC EFFECTS OF HY
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                                                                                                                           gamma
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ne EMBL/GenBank/DDBJ databases
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Pred. No. 6.9;
3; Mismatches
                                                                                                                                                                                                            Last
                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB Pred. No. 9.5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heijnen L.,
                                                                                                                                                                                                                                                      PRT;
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                                                                                                                           subdivision; Pseudomonadaceae;
                                                                                                                                                                                                              sequence
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9.5;
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    HYDROGEN
                 ORGANISMS
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Q9RNU2 PRELIMINARY; PKI; 210 AAA
Q9RNU2;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-MAY-2000 (TrEMBLrel. 13, Last annotation
SERUM OPACITY FACTOR PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-MAASTRICHT;
STRAIN-MAASTRICHT;
MEDLINE-20473137; PubMed-11018281;
MEDLINE-20473137; PubMed E., Bruggeman
Gruijthuijsen Y.K., Beuken E., Bruggeman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09DWH8;
01-MAR-2001
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                        "Rat cytomegalovirus R89 is spliced transcript."; Virus Res. 69:119-130(2000). EMBL; AF232689; AAF99111.1; SEQUENCE 1240 AA; 125612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; pF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
Probom; PD000510; Catalase; 1.
PROSITE; PS00438; CATALASE_2; 1.
PLASMId; OXIGOTEGUCCLASE; PETOXIDASE; Iron; Heme; Hydroraction of the catalase; PS064A; 57324 MW; F1EAA728C5D41CBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -I- CATALYTIC ACTIVITY: 2 H(2)O(2) - O(2) + 2 H(2)O.
-I- COFACTOR: HEME GROUP.
EMBL; U72068; AAB17009.1; -.
HSSP; P4231; 2CAE.
InterPro; IPR002226; Catalase.
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-MAASTRICHT;
MEDLINE-20366325; PubMed-10906222;
Vink C., Beuken E., Bruggeman C.A.;
"Complete DNA sequence of the rat cytomegalovirus J. Virol. 74:7656-7665(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                   Betaherpesvirinae; Muromegalovirus.
NCBI_TaxID=79700;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat cytomegalovirus (strain Maastricht).
Viruses; dsDNA viruses, no RNA stage; He
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01-MAR-2001
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                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=SS1401 TYPE PT1658; Beall B., Gherardi G.;
                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence up
01-NOV-1999 (TrEMBLrel. 12, Last annotation
01-NOV-1999 (TrEMBLrel. 12, Last annotation
SERUM OPACITY FACTOR PRECURSOR (FRAGMENT).
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STRAIN=4470-96; TISSUE=BLOOD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Streptococcus.
                                                                                                                                                                                                          "The relation of Streptococcus pyogenes sof and types to genetically distinct strain sets."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ da EMBL; AF154330; AAD36988.1; -.
                                                                                                                                                                                                                                                                                             Streptococcus.
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211 AA;
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57.1%;
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Pred. No.
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SERUM OPACITY FACTOR
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SERUM OPACITY FACTOR
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01-MAY-2000
01-JUN-2001
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Submitted (OCT-1999) to
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NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                            CATALASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro, IPR000782; BIGH3_fasciclin
InterPro; IPR000073; NMT.
Pfam; PF02469; Fasciclin; 1.
PROSITE; PS00976; NMT_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EU Arabidopsis sequencing project;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ
EMBL; AL132972; CAC07928.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alcaraz J.P., Clabault G., Cottet A., Mache R., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat Submitted (NOV-1999) to the EMBL/GenBank/DDBJ dd
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eddicotyledoms; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                     the
                                                                                          Redenbach M., Kieser H.M.,
Kinashi H., Hopwood D.A.;
                                                                                                                                                                            STRAIN=A3(2);
Thomson N.R.,
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Murphy L., Ha
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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T25B15_140.
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 EMBL;
                                                                                                                    MEDLINE=97000351; PubMed=8843436;
                                                                                                                                 STRAIN=A3(2);
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           set of ordered cosmids and a detailed 8 Mb Streptomyces coelicolor A3(2) ch. Microbiol. 21.77-96(1996).
FUNCTION: OCCURS IN ALMOST ALL AEROBI SERVES TO PROTECT CELLS FROM THE TOXI PEROXIDE (BY SIMILARITY).
CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2)
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EC 1.11 1.6).
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CTIVITY: 2 \text{ H}(2)\text{O}(2) = \text{CAB58320.1};
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17, Last annotation updat
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PRINTS; PR00067; CATALASE.
ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
Heme; Hydrogen peroxide; Iron; Oxi
SEQUENCE 487 AA; 55116 MW; 9D3
                         Q54272
Q54272;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
        Streptomyces hygroscopicus
                    HYPOTHETICAL ALDEHYDE-DEHYDROGENASE (EC 1.2.1.-).
                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                              Submitted (OCT-1999) to the EMBL; AF198626; AAF15285.1; HSSP; P38636; ICC8. Interpro; IPRO1934; HMA.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                                                      InterPro; IPRO
Pfam; PF00403;
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=98399102; PubMed=9701579;
Himelblau E., Mira H., Lin S.J., 'Amasino R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COPPER CHAPERONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9SE04;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9SE04
                                                                                                                                                                                                                                                                                                                    Mira H.,
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                      Plant Physiol.
                                                                                                                                                                                                                                                                                                                                                    "Identification of a functional homolog homeostasis gene ATX1 from Arabidopsis. Plant Physiol. 117:1227-1234(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                        'Copper chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P42321;
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                                                                                                                                            97
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                                                                                                                                            EAAPPTTTAAEAPAIAAA 114
                                                                                                                                                                 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLTTVAGAPVPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLTTAAXAPVVXN
                                                                                                                                                                                       Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                       Penarrubia L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR002226; Catalase
Firmicutes; Actinobacteria;
                                                                                                                                                                                                                                             403; HMA;
132 AA;
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2CAE
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13094 MW;
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69
                                                                                                                                                                                                                                                                                                                                                                            functional homolog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCH.
                                                                                                                                                                                       1;
                                                                                                                                                                                                Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                            sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oxidoreductase; Peroxidase 9D3334889EAF60B7 CRC64;
                                                                                                                                                                                                                                           7176EF95350A8231
                                                                                                                                                                                       Mismatches
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Actinobacteridae;
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a; Poales; Poa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 487
                                                                                                                                                                                                           Length 132;
                                                                                                                                                                                                                                              CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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8
        Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
KA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
KA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
KA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
KA Sutton G.G., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Ghoreva D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gebblos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubbrt W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kammel B.E., Kodlra C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kammel B.E., Kodlra C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lia X., Mattel R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 9
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01-MAY-2000 (Tre)
01-JUN-2001 (Tre)
CG18373 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               blalaphos-producing Streptomyces hygrosc

Gene 138:149-150(1995).

-I- PATHMAY: BILLAPHOS BIOSYNTHESIS.

-I- SIMILARITY: BELONGS TO THE ALDEHYDE

EMBL: D37877; BAA07116.1; -.

HSSP; P05091; 1CW3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ephydroidea; Dro
NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Oxidoreductase.

ACT_SITE 187 187 BY SIMILARITY.

ACT_SITE 221 221 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00171; aldedh; 1. PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95309717; PubMed-7789803;
Hidaka T., Hidaka M., Kuzuyama T., Seto H.;
"Sequence of a P-methyltransferase-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
NCBI_TaxID=1912;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002086; Aldehyde_dehydr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKTPLTALAFAELLIEA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces hygroscopicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43406 MW;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB Pred. No. 31; 2; Mismatches
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  McLeod
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cus.";
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                                                          K.A.,
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RESULT 14
Q9U3E3
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Best Local
                                                   Matches
                                                              Query Match
Best Local
                                                                                                        Investigating biology.;
Science 282:2012-2018(1998).
EMBL; Z82273; CAB54978.1; -.
InterPro; IPR003127; Sorb.
SMART; SM00459; Sorb; 1.
SEQUENCE 171 AA; 18844 MW;
                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000
01-MAY-2000
01-JUN-2001
F56F12.1 PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).

EMBL: AE003813; AAF58220.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Patlazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T., Stope B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0033956; CG18373.
InterPro; IPR002052; N6_Mtase.
PROSITE; PS00092; N6_MTASE; UN
                                                                                                                                                                                                                          MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                Submitted (APR-1999)
                                                                                                                                                                                                                                                                             Ainscough
                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                         F56F12
                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9U3E3;
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                                                                                                                                                                                                            none;
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
                                                                                                                                                                                               "Genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    695 EEVTPYNTAPHSPIV 709
73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N
                        5 TPLTTAAXAPVVXNA 19
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 TPTTTAAAPIAAVA
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8; Conser
                                                8; Conservative
                                                                                                                                                                                                                                                                                         FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                ) (TrEMBLrel.) (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1012 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                               of the nematode
                                                                                                                  18844 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.6%;
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13,
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MW; 5CF624239372C936 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB Pred. No. 76; 2; Mismatches
                                                               Score 40;
Pred. No.
                                                                                                                  D782482A786F7941 CRC64;
                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  sequence update)
annotation updat
                                                                                                                                                                                               C.elegans: A platform
                                                                                                                                                                                                                                                                                                                                                                                                                                                     171
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76;
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19;
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                                                   6:
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                                                                           Length 171;
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                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Moshreft A.
                                                                                                                                                                                                 for
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                                                   0;
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                                                   Gaps
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RESULT 15 Q9U4Y3 ID Q9U4Y3

PRELIMINARY;

PRT;

212

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Search completed: February 28, 2002, 11:39:33 Job time: 334 sec
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 49.4
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                              InterPro; IPR000210; BTB_POZ.
Pfam; PF00651; BTB; 1.
PROSITE; PS50097; BTB; 1.
SMART; SM00225; BTB; 1.
NON_TER 212 1 1
NON_TER 212 AA; 22715 MW;
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Davis T., Yamamoto D.;
Davis T., Yamamoto D.;
"Sequence of the fruitless gene in Ceratitis capitata.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF124047; AFF22527.1;
TEMBL, AF124047; AFF22527.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ceratitis capitata (Mediterranean fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Tephritoidea; Tephritidae; Ceratitis.
NCBI_TaxID=7213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9U4Y3;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
FRUITLESS PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRU.
                                                                                      188 ERSPLTAAAMAAAVAAA 204
                                                                                                          3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                 212 212
212 AA; 22715 MW;
                                                                                                                                                         49.4%; Score 40; DB 5; 52.9%; Pred. No. 24; tive 2; Mismatches
                                                                                                                                                                                                                                                 D1B7C38FBC5AB8AB CRC64;
                                                                                                                                                                                         Length 212;
                                                                                                                                                             6; Indels
                                                                                                                                                           0; Gaps
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                      Query
Match Length
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1: /SIDS8/qcadate
           BLOSUM62
Gapop 10.0 , Gapext 0.5
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48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           522463 seqs, 74073290 residues
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Copyright (c) 1993 - 2000 Com
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/SIDSB/gcgdata/geneseq/geneseqp/AA1990.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT:*
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AAB69062
AAB95523
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AAW53264
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AAG23995
       AAG23994
AAG70918
AAG23993
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Sequence of human Human p154. Homo Human adipocyte-sp Human adipocyte-sp Arabidopsis thalia Arabidopsis thalia C albicans apoptos Arabidopsis thalia
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418	418	418	418	418	418	418	418	418	418	418	411	393	350	344	339	314	292	291	257	240	159	149	121	115	108	108	108	108	77	65	1786	1558	478
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AAB60264	AAY70680	AAY96247	AAY95285	AAY95976	AAW94472	AAW97769	AAY05514	AAY05858	AAW61486	AAR77340 .	AAY37272	AAU04046	AAE05988	AAB73609	AAW20275	AAE06570	AAG30090	AAG30091	AAB18340	AAG81209	AAG04659	AAG04660	AAG93027	AAB27999	AAY98226	AAY95117	AAW01265	AAR54307	AAG59122	AAG59124	AAW24790	AAB18324	AAB31971
Sonic	afis	al zebrafis	fish Soni		h Shh	Sonic	Sonic	h Sonic	sonic	-	Amino acid sequenc	Streptococcus coel	Clostridium diffic	Sphingobacterium s	H. pylori cytoplas	Schisandra chinens		Arabidopsis thalia	Plasmodium falcipa	c		Arabidopsis thalia	C glutamicum prote	an secre	i-gp120	i-gp120 an	region o	$\vdash$	thal	bidopsis th	P. falciparum live	modium falc	Rice glutamate 1-s

## ALIGNMENTS

RESULT

AAW64480 standard; peptide;

19 ΑA

AAW64480;

20-OCT-1998

(first entry)

(AUSP-) AUSPHARM INT LTD. (CHAP/) CHAPMAN P W. 30-JUL-1998. Misc-difference Misc-difference Misc-difference 24-JAN-1997; 26-JAN-1998; WO9832769-AI Pseudomonas aeruginosa. Antigen; Pa60; diagnosis; detection; cystic fibrosis; vaccine; P. aeruginosa protein antigen Pa60 N-terminal peptide fragment immunogen; infection; treatment. 97GB-0001489 98WO-GB00217 /label≃ unknown 12 Location/Qualifiers /label= unknown 'label= unknown

Clancy RL,

Cripps AW,

Dunkley M,

Kyd

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This peptide is the N-terminal fragment of a novel foundamonas aeruginosa protein antigen, Pa60. This fragment could be used for diagnostic detection of P. aeruginosa by forming complexes with specific antibodies, particularly in patients with cystic fibrosis (by analysis of mucus, e.g. in saliva), or in vaccines or immunogenic compositions to treat or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein antigen from Pseudomonas aeruginosa and its antigenic
fragments - useful diagnostically to detect specific antibodies
particularly in patients with cystic fibrosis, and as vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                    and/or
                                                                                                                                                                03-JUL-2000;
                                                                                                                                                                                     11-JAN-2001
                                                                                                                                                                                                         WO200102577-A1.
                                                                                                                                                                                                                                       Misc-difference
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                                                                                                                                                                                                                                                                                                             Pseudomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prevent infection by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                         against P.
                                                            Antigenic Pseudomonas aeruginosa proteins,
                                                                                 WPI; 2001-080988/09.
                                                                                                     Smith CJ,
                                                                                                                         (PROV-) PROVALIS UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                   diagnosis of P. aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                         standard; | peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 2; 23pp; English
                                                                                                   Thompson
                                        aeruginosa
                                                                                                                                                                                                                                                                                                                                detection;
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                                                                                                                                                                                                                                                                                                            aeruginosa
                                                                                                                                                                                                                                                                                                                                          aeruginosa;
                                                                                                                                                                                                                                                                                                                                                             aeruginosa protein N-terminal
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D.

Disclosure;

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129pp;

English

present

invention Page

describes antigenic

Pseudomonas

aeruginosa

polynucleotide sequence and

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RESULT
AAB95523
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteins (P1). The P. aeruginosa proteins have antibacterial activity and can be used in vaccines and as antagonists. The proteins or their fragments, or antibodies are useful in the detection and/or diagnosis of P. aeruginosa. They are also useful for producing a vaccine and inducing an immune response against P. aeruginosa infection. An agent capable of antagonising, inhibiting or otherwise interfering with the function or expression of P1 are useful in the manufacture of a medicament for the treatment or prophylaxis of P. aeruginosa infections. The present sequence represents a probable P. aeruginosa protein N-terminal nontified semimora from the present invention
                                                                                                                                                                                                                                                                                                                                                       29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                    The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5 -end
                                                                                                                                                                                                                                                        WPI;
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                                                                                                                                                      Claim
                                                                                                                                                                                                full-length cDNAs define and/or diagnosis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUN-2001
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10; Conserv
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                                                                                                                                                                                                                                                                                                                            HELIX RES
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Sugiyama T, Wakamats
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                                                                                                                                                                                              for synthesizing polynucleotides, particularly the 5602 cDNAs defined in the specification, and for the detections of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                        99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
an oligonucleotide comprising a sequence de which comprises a 3'-end sequence, when
                                                                                                                                                        ID 18106;
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A, Nagai K,
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, Otsuki
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                                                        or (b) a combination
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                to
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Sequence

892 AA;

0

the present invention.

detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification

oligonucleotide comprises at least 15 nucleotides and the combination of the 5-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides particularly full-length cDNAs. The primers are also useful for the

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 5; Conser
this cell line was discovered and termed protein 154 or p154. It is expressed in high quantitites in adipogenic cell lines only after cell differentiation; it its abundant in the fat pads of normal and genetically obese mice; and its expression is 3 to 5 fold higher the fat pads of obese animals compared to the fat pads of their littermates. A human fat cell cDNA library was hybridisec with a 405 bp cDNA including the 5' end of mouse p154. The positive plaques were sequenced. Clone B&B yielded DNA of 450 bp of which
                                                                                                                                                       Adipose differentiation was studied using a C3H mouse teratoma-derived cell line called 1246 is bipotential, able to differentiate into adipocytes and also muscle cells. A ZAP CDNA library was constructed from fully differentiated 1246 cells. A novel adipocyte-specific polypeptide encoded by the DNA and mRNA
                                                                                                                                                                                                                                                                                                                                   DNA encoding human or mouse adipocyte polypeptide p154 - and RNA mols. encoding p154 are used for determining susceptibility to
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-404011/50.
N-PSDB; AAQ54135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence of human adlpocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR45152 standard; Protein; 148
                                                                                                                                                                                                                                                                        Disclosure; columns 41-42; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Serrero G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ALTO-) ALTON JONES CELL SCI CENT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-DEC-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5268295-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adipocyte polypeptide; p154; protein 154; obesity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR45152
                                                                                                                                                                                                                                                                                                               obesity and evaluating anti-obesity drugs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide (ap) p154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 23; DB 22;
Pred. No. 5.6e+02;
3; Mismatches 10
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Query Match Best Local S Matches 5

Similarity 27.8 5; Conservative

45.8%; 27.8%;

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Best Local
                                                                                                  The present sequence is that of human p154. The p154 mRNA is expressed in high quantities in adipogenic cell lines only after cell differentiation. The murine p154 mRNA is abundant in the fat pads of normal and genetically obese mice and its expression is 3 - to 5 fold higher in the fat pads of obese animals compared to the fat pads of their normal littermates. The DNA sequences (AAT4455-46) can be used to provide probes or for recombinant production of p154. The protein can be used for generation of antibodies. Both antibodies and probes can be used to determine the susceptibility of a subject to obesity. Also efficacy of anti-obesity drugs can be evaluated by contacting the drug to be tested with an adipocyte in vitro and measuring the amt. of p154 or mRNA produced, the efficacy of the drug being proportional to the decrease in the produ. of the polypeptide or mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            474 bp contained the coding region of the human p154 DNA. Homology with the mouse p154 cDNA started at AA 50 and continued to AA 197, with 798 homology.
                                                                                                                                                                                                                                                                                                                  Claim 4;
                                                                                                                                                                                                                                                                                                                                              Mammalian adipocyte p154 polypeptide and related antibodies - useful in immunoassays to assess susceptibility to obesity
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-361954/36.
N-PSDB; AAT44456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAY-1991;
22-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p154; murine; human; anti-obesity; drug evaluation; probe; antibody; susceptibility; adipocyte; efficacy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW06799;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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5; Conser
                                                                                                                                                                                                                                                                                                                    Column 39-40;
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93US-0127995
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27.8%;
                                                                                                                                                                                                                                                                                                                 32pp; English.
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Score 22; DB
Pred. No. 1.6e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 22; DB 14;
Pred. No. 1.6e+02;
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               DB 17;
1.6e+02;
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RESULT
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AC AAY9
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AC AAY9
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                                                                                                                                                                                       Query Match
Best Local S
                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                         The present sequence represents human adipocyte-specific differentiation related protein (HADRP). The DNA and protein may be used to treat or diagnose disorders of lipid metabolism, e.g. obesity, diabetes, hypercholesterolaemia or hyperlipidaemia, or to treat cancer.
 Human adipocyte-specific differentiation-related protein
                                                                                                                                                                                                                                                                                                                                          Human adipocyte-specific differentiation-related protein - useful for, e.g. diagnosing or treating disorders of lipid metabolism such as obesity
                        27-OCT-2000
                                               AAY99534;
                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                   Claim 1; Column 31-34; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; adipocyte-specific differentiation-related protein; HADRP; Lipid metabolism; obesity; diabetes; hypercholesterolaemia;
                                                                      AAY99534 standard;
                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAV20862.
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-260032/23.
                                                                                                                                                                                                                                                                                                                                                                                                                          Hawkins PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-APR-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hyperlipidaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human adipocyte-specific differentiation-related protein.
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                         (first
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/note= "encoded
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                                                                     Protein; 437
                         entry)
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27.8%;
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                                                                                                                                                                            Score 22; DB 19
Pred. No. 5e+02;
3; Mismatches
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Best Local S
Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying a substance for treating or preventing a viral infection such as hepatitis C virus, comprises determining if the substance disrupts a lipid globule target sequence to lipid globule interaction
                                                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                   Arabidopsis thaliana
                                                                                                              Arabidopsis thaliana protein fragment SEQ ID NO:
                                                                                                                                          17-OCT-2000
                                                                                                                                                                   AAG23995;
                                                                                                                                                                                          AAG23995 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                        Sequence
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Misc-difference
                                                               termination sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; adipocyte-specific differentiation-related protein; ADRP; lipid globule; chronic hepatitis; liver disease; ADRP displacement.
                                                                                                                                                                                                                                                                                                          Local Similarity 27.1 tos 5; Conservative
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DB; AAA46136.
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                                                                                                                                                                                                                                                                                                                                                                        437
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                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                        AA;
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27.8%;
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Pred. No.
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908-01 908-01 908-01 908-01 908-01 908-01 908-01	99US-0132407. 99US-0132484. 99US-0132486. 99US-0132486. 99US-0132486. 99US-0132486. 99US-0134256. 99US-0134219. 99US-0134768. 99US-0135124. 99US-0135124. 99US-0135124. 99US-0135629. 99US-0135353. 99US-0135629. 99US-0137528. 99US-0139454. 99US-0139454. 99US-0139454. 99US-0139456. 99US-0139456.	DEP-031
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908-01 908-01 908-01 908-01 908-01 908-01 908-01	9908-0145083 9908-0145087 9908-0145189 9908-0145145 9908-0145121 9908-0145218 9908-0145918 9908-0146386 9908-0146386 9908-014708 9908-014708 9908-0147192 9908-0147192 9908-0147416 9908-01474192 9908-01474192 9908-01474192 9908-01474192 9908-01474192 9908-014811 9908-014811 9908-014811 9908-014811 9908-014811 9908-014811 9908-014918 9908-014918 9908-014918 9908-014918 9908-014918 9908-014918 9908-014929 9908-014929 9908-014929	US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US-011 US

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24-SEP-1999;
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                                                                                                              Arabidopsis thaliana.
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Similarity 33.3%;
6; Conservative
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                                               2000EP-0301439
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99US-0123548.
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Pred. No. 2.6e+02;
1; Mismatches 11;
                                                                                                                                             al transduction pathway; metabolic pathway;
mapping; gene expression control; promoter;
                                                                                                                                                                             fragment
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RESULT 10
AAG70918
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AC AAG709
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XX
DE C alb
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PR 01-:
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08-0CT-1999;
12-0CT-1999;
13-0CT-1999;
13-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                    Candida albicans.
                                                                                                                                                                                                                                                                                                                                                                                         Yeast; fungus; apoptosis; infection; proliferative disease; vaccine; autoimmune disease; ischaemla; neurodegeneration.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG70918 standard;
                                      WPI; 2001-367042/38.
N-PSDB; AAH29954.
                                                                                              Contreras RH,
Nelissen BJM,
                                                                                                                                                                                           01-JUL-1999;
                                                                                                                                                                                                                                 03-JUL-2000; 2000WO-BE00077.
                                                                                                                                                                                                                                                                        11-JAN-2001
Yeast and fungal nucleic acids encoding proteins involved in
                                                                                                                                                                                                                                                                                                              WO200102550-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JUL-2001
                                                                                                                                                     (JANC ) JANSSEN PHARM NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 eekatkavqclnemvtna
                                                                                                                                                                                                                                                                                                                                                                                                                                                 albicans apoptosis associated
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9908-0158223

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9908-0159331

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9908-0159637

9908-0160741

9908-0160774

9908-0160770

9908-016078

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                                                                                                De Backer
Reekmans F
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; Pred. No. 2.7e
1; Mismatches
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                                                                                                                Luyten WHML,
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                                                                                                                  Malcorps IKL;
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    a pathway
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RESULT 11
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disorders,
certain dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of a number of apoptosis associated proteins from the yeast Saccharomyces cerevisiae and the fungus Candida albicans. These can be used to identify treatments for fungal and yeast infections, for proliferative diseases and for apoptosis related diseases such as autoimmune diseases, ischaemia and neurodegeneration. The present sequence is one of the C. albicans proteins of the invention.
                                                                                                                                                                                                                                          25-FEB-2000;
                                                                                                                                                                                                                                                           06-SEP-2000
                                                                                                                                                                                                                                                                              EP1033405-A2
                                                                                                                                                                                                                                                                                                                hybridisation assay; termination sequence.
                                                                                                                                                                                                                                                                                                                                  Protein identification;
                                                                                                                                                                                                                                                                                                                                                                       17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                          AAG23993 standard; Protein; 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                              Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO:
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                     (first
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990S-0121825

990S-0125788

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990S-0126785

990S-0127462

990S-0128234

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990S-0128214

990S-0128214

990S-0130810

990S-0130810

990S-013149

990S-0132484

990S-0132487

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Pred. No. 3.1e+02;
1; Mismatches 10
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mapping; gene expression control; promoter;
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05-OCT-1999;
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The present sequence represents a glutamate 1-semialdehyde (GSA) aminotransferase which is an aminolevulinic acid biosynthetic enzyme. Glu-tRNA reductase converts Glu-tRNA-Glu to GSA with the concomitant release of tRNA-Glu. GSA aminotransferase then converts GSA to 5-aminolevulinic acid (ALA). ALA is used in the biosynthesis of tetrapyrrolic pigments such as chlorophyll. Nucleic acids encoding aminolevulinic acid biosynthetic enzymes are useful for isolating cDNA and genes encoding homologous proteins from the same or other plant species, for creating transgenic plants in which the polypeptides are present at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glu-tRNA reductase; aminolevulinic acid; tetrapyrrolic pigment; chlorophyll; trans 1-semialdehyde aminotransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rice
                                                                                                                                                                 New nucleic acids encoding an aminolevulinic acid biosynthetic enzyme useful for producing large amounts of the encoded polypeptides used in screening compounds for potential herbicidal activity \,
                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
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N-PSDB; AAF54825.
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                                                                                                  Also described are: (1) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II). (I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify are resistance in the latent or they can be used to identify a registance in
                                        P. falciparum. Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for
                                                                                                                                                                                                                                                                                                                  Proteins encoded by chromosome 2 of the human Plasmodium falciparum, useful as antimalarial diagnosis of P.falciparum infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         large amounts of the encoded polypeptides which could then be used for screening different compounds for potential herbicidal activity, and as hybridisation probes and amplification primers.
              vaccine and drug development. Parasite resistance to drugs and resistance to insecticides have led to a resurgence of malaria
                                                                                                                                                                                                                                                                                        Disclosure;
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(CARU/) CARUCCI D.
(GARD/) GARDNER M.
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                                                                                                                                                                                                                                         present invention describes proteins and their fragments (I) encoded chromosome 2 of the human malarial parasite, Plasmodium falciparum.
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                                                                This sequence corresponds to a Plasmodium falciparum strain K1 pre-erythrocytic liver stage antigen 3 (LSA-3) protein. The encoding gene sequence was isolated by screening a P. falciparum strain T9/96 library with serum from a missionary treated by prophylaxis (for strain T6/96 see FR9101286). Of 20 clones isolated, clone 729S was used to screen a library generated from Thai strain K1. One clone contained a 6.85 kb insert including the genomic sequence AAT78867. The gene comprises a 1.8 kb region encoding 3 major blocks of tetraperbide
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                                                                                                                                                                                                                                                                                                       Claim 1;
                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum poly:peptide(s) and related nucleic acids -derived from the liver stage antigen-3, useful for malaria vaccine
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Pred. No. 3.6e+03;
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repeats (especially the amino acid sequence VEES, etc) and a 3' hydrophobic region corresponding to

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hybridisation assay; genetic mapping; gene expression control; promoter;
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PR 05-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147363.
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PR 09-AUG-1999; 99US-0147413.
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PR 22-AUG-1999; 99US-015086.
PR 27-AUG-1999; 99US-015108.
PR 28-AUG-1999; 99US-016108.
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PR 28-AUG
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Search completed: February 28, 2002, 11:34:38 Job time: 74 sec

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US-08-676-444-44	US-09-109-916-60	US-08-511-485-13	US-08-468-059-60	US-08-471-770-60	US-08-470-202-60	US-09-457-046B-59	US-09-216-294-1	US-08-923-856-1	US-08-247-491A-5	US-08-468-718-4	US-08-467-852A-5	US-08-214-222-4	US-08-469-434-4	US-08-072-070-4	90-	US-08-312-949-4	US-07-929-198-4
44	•	•	•	Sequence 60, Appl	60,	59	Sequence 1, Appli	<u>-</u>	Sequence 5, Appli	4	ۍ.	Sequence 4, Appli	Sequence 4, Appll	Sequence 4, Appli	Sequence 4, Appli	4	Sequence 4, Appli

## ALIGNMENTS

MAMMALIAN ADIPOCYTE PROTEIN, ACIDS CODING
THEREFOR AND USES THEREOF

NUCLEIC

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US-07-708-038-4
                                                                        Query Match
Best Local s
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 419 Seventh Street, NW
CITY: Washington
STATE: DC
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.25
                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                         TELEFAX: 202-737-3528 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Livnat, Shmuel
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: SERR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPHONE: 202-727-258-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Serrero, Ginette
TITLE OF INVENTION: MANMALIAN ADIP
TITLE OF INVENTION: ACIDS CODING
TITLE OF INVENTION: THEREFOR AND U.
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Browdy and Neimark
STREET: 419 Seventh Street, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19910531
45 EERLPILNOPSTOIVANA 62
                                2 EEKXXLXXXXXXXVVXNA 19
                                                                      Similarity 27.8
5; Conservative
                                                                                         45.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/07/708,038
                                                                      Score 22; DB Pred. No. 66; 3; Mismatches
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                                                                                                           <del>-</del>-
                                                                        10;
                                                                                                           Length 148
                                                                        Indels
                                                                    0;
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-127-995-4
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US-08-127-995-4
                                                                                                                                                                                                                                                                                                                   US-08-764-343-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08127995 Patent No. 5541068
                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08764343 Patent No. 5739009
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                      GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET, NUMBER: SE
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 31-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                   APPLICANT: Hillman, Jennifer L.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL ADIPOCYTE-SPECIFIC
TITLE OF INVENTION: DIFFERENTIATION-RELATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: LC
STATE: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                   STREET: 51.
                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/01 FILING DATE: 15-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/708,038 FILING DATE: 31-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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                                                                                                                                                                                                                                                                                                                                                                                    45 EERLPILNQPSTQIVANA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                              COUNTRY:
                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                 2 EEKXXLXXXXXXXVVXNA 19
                                                                    94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington
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                                                                                   US
                                                                                                                                 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 amino acids
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202-737-3528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                    INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G. Kevin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.8%;
27.8%;
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Pred. No.
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US-08-764-343-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application Patent No. 5989820 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,
FILTHO NUMBER: US/08/764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bandman, OLYGA
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN ADIPOPHILIN-LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                APPLICATION NUMBER:
FILING DATE:
ATTORNEY_AGENT INFORMATION:
ATTORNEY_BILLINGS THOSE TO THE TOTAL THE TOTAL TO THE TOTAL THE TOTAL TO T
                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
                                     REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 31/.
CTTY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 EERLPILNQPSTQIVANA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                         NAME: Billings, Lucy J
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 EEKXXLXXXXXXXXVVXNA 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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27.8%;
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                                                                                                                                            36,749
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                                                                                                           PF-0440 US
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Pred. No. 2e+02;
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INFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS:

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US-08-973-462-9
                                                                                                                                                                                                                                                                                         US-08-973-462-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-989-925-3
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Best Local Similarity 2/..
Thes 5; Conservative
                                                                                                                                                                                                                                                    Sequence 8, Application US/08973462B Patent No. 6191270
                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 9
LENGTH: 630
                CURRENT APPLICATION NUMBER: US/08/973.462B
CURRENT FILING DATE: 1998-02-06
EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER FILING DATE: 1996-06-12
EARLIER APPLICATION NUMBER: FR 95/07007
EARLIER APPLICATION NUMBER: FR 95/07007
EARLIER FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
FILE REFERENCE: 0660-0125-0 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: DRUILHE, PIERRE
APPLICANT: DAUBERSIES, PIERRE
APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
FILE REFERENCE: 0660-0125-0 PCT
CURRENT APPLICATION UMBER: US/08/973,462B
CURRENT FILING DATE: 1998-02-06
EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER FILING DATE: 1996-06-12
EARLIER FILING DATE: 1996-06-13
NUMBER OF SEQ ID NOS: 29
VUMBER OF SEQ ID NOS: 29
SOPTMARE: PALEORLIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/08973462B
Patent No. 6191270
                                                                                                                                                                                                             APPLICANT: DRUILHE, PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                      593 EEKVDLNENVVSSILDN 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 29.4 nes 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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CLONE: 1806040
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                                                                                                                                                                                                                                                                                                                                                                                                             2 EEKXXLXXXXXXXVVXN 18
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Patentin Ver. 2.0
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Pred. No.
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Pred. No.
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5.3e+02;
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Best Local Similarity 25...
Thes 5; Conservative
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LENGTH: 1786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 86,
                                                                                       TELEFAX: 619-554-6312 INFORMATION FOR SEQ ID NO:
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                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                         FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                          TYPE: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220, STREET: Mail Drop TPC8
                          TOPOLOGY:
                                                                                                                                              REGISTRATION NUMBER: 34 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 30-SEP
                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 18-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
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                                       : 108 amino acids
amino acid
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                                                                                                     619-554-6312
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                            linear
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SYSTEM: PC-DOS/MS-DOS
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            protein
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Carlos F
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                                                                                     86:
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Pred. No.
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Query Match
Best Local Similarity
Matches 4; Conserv

Conservative

41.7%; 25.0%;

Score 20; DB 1; Pred. No. 1.7e+02 2; Mismatches 1:

Length 108

Indels

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ERATLSCRASQSVISN

Carlos F

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RESULT 8
US-08-899-575-86
             US-08-899-575-86; Sequence 86, Applicat; Patent No. 5804440; GENERAL INFORMATION:
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                                                                             RESULT
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                                                                                                                                                                                                           Query Match
Best Local
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 30-SEP-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 30-SEP-PRIOR APPLICATION DATA:
APPLICANT:
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STATE: CA
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                                                                                                                          15 ERATLSCRASQSVISN 30
                                                                                                                                                                                        Local Similarity
ses 4; Conser
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                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/954,148
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                                                                                                                                                         3 EKXXLXXXXXXXVVXN 18
                                                                                                                                                                                                                                                                                                              amino acid
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                                            Application US/08899575
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HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TO HUMAN IMMUNODEFICIENCY VIRUS
 Dennis
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25.0%;
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                                                                                                                                                                                                                        Score 20;
                                                                                                                                                                                                           Pred. No. 1.7e+02
                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                         DB 1;
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RESULT 10
PCT-US95-08743-86
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Best Local Similarity 25.0
                                                                                                                                                                                                              Sequence 86, Application PC/TUS9508743 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 0
FILING DATE: 18-JUL-1994
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PRIOR APPLICATION DATA:
                                                                                                             NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                               TITLE OF INVENTION:
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SOFTWARE: Patentl
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             APPLICATION NUMBER: PCT/US95/08743 FILING DATE: 11-JUL-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                  41.7%;
25.0%;
                                                                                                                                                               HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 20;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCR1452P
                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                 Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 108;
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В

FILING DATE: 18-JUL-1

86:

APPLICATION NUMBER: US 08/276,852 FILING DATE: 18-JUL-1994

SEQUENCE CHARACTERISTICS: LENGTH: 108 amino acid

108 amino acids

TYPE: amino acid

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Query Match
Best Local Similarity
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Best Local S
Matches 4
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Sequence 63, Application US/08946329A
Patent No. 6057091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                           TELEPHONE: 619/678-50 TELEFAX: 619/678-5099 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/946,329A FILING DATE: 07-OCT-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/061,323 FILING DATE: 07-OCT-1996 APPLICATION NUMBER: 08/729,743 FILING DATE: 10-JUL-1996
                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Beachy, Philip A.
APPLICANT: Porter, Jeffrey A.
TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 619/678-5070
                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                           NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/140001
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/567,357
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/349,498
FILING DATE: 02-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: La Jolla
STATE: CA
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                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                            LENGTH:
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                                                                                                                                                            148 amino acids
               Conservative
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             Score 20; DB 3; ....
Pred. No. 2.3e+02;
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Pred. No. 1.7e+02;
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                                               Length 148;
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US-08-176-427B-10
                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                            Sequence 10,
                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:

APPLICATION NUMBER:

US/08/176,427B

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

STATE: STREET:

MA

COUNTRY: CITY: Boston

USA

02109

NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD

60 State Street

TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto

APPLICANT: Ingham, Phillip W. APPLICANT: McMahon, Andrew P. APPLICANT: Tabin, Clifford J.

0, Application US/08176427B 5789543

181 QEKVALFGDGEAKVIWN 197

2 EEKXXLXXXXXXXVVXN 18

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Query Match
Best Local Similarity
"hehes 5; Conserv
                                                                                                           ; ORGANISM: Schisandra chinensis US-09-475-316A-118
                                                                                                                                                                                SOFTWARE: P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 118, Application US/09475316A Patent No. 6210942
                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: PCT/US97/20
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: 60/054,380
PRIOR FILING DATE: 1997-07-31
PRIOR FILING DATE: 1997-07-31
                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1996-1
                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/475,316A CURRENT FILING DATE: 1999-12-30 PRIOR APPLICATION NUMBER: 09/307,653
                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: RECOMBINANT PINORESINOL/LARICIRESINOL REDUCTASES. TITLE OF INVENTION: RECOMBINANT DIRIGENT PROTEINS AND METHODS OF USE FILE REFERENCE: WSUR-1-13793
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TYPE: PRT
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                 Conservative
                                                                                                                                                                                                                                     1996-11-08
                                    41.78;
29.48;
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                                    Score 20; DB 4;
Pred. No. 4.9e+02;
                   Mismatches
                                                     Length 314;
                   0;
                   Gaps
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Best Local Similarity
Whiches 5; Conserv
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US-08-356-060A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/08356060A Patent No. 5844079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 418 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617) 227-59
INFORMATION FOR SEQ ID NO:
                                                                                           TELEFAX: (617) 227-5941
NFORMATION FOR SEQ ID NO: 12:
                                                                                                                          FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006CP
TELECOMMUNICATION INFORMATION:
TELECHONE: (617) 227-7400
                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 418 amino acid
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Induc
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006
TELECOMMUNICATION! INFORMATION:
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NAME: Vincent, Matthew P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 EKITLTAAHLLFYLDNS 278
                            TYPE: amino acids
                      TOPOLOGY:
                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/176,427 FILING DATE: 30-DEC-1993
                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 14-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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CLASSIFICATION: 435
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                     linear
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IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (617) 227-7400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             227-5941
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29.4%;
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Pred. No. 6.6e+02;
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US-08-946-329A-18
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Best Local Similarity
"~* hes 5; Conserv?
                                                           Matches
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                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                COURMENT AFFECTION NUMBER: US/08/940, DEPLICATION NUMBER: US/08/940, DEFILING DATE: 07-0CT-1997
PRIOR APPLICATION DATA:
PARTON NUMBER: 60/061,323
                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                            FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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STREET:
CITY: La Jo.
CITY: CA
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Beachy, Philip A. APPLICANT: Porter, Jeffrey A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
262 EKITLTAAHLLFVLDNS 278
                                                          Local Similarity hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262 EKITLTAAHLLFVLDNS 278
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/061,323
FILING DATE: 07-OCT-1996
APPLICATION NUMBER: 08/729,743
                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 10-JUL-1996
APPLICATION NUMBER: 08/567,357
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/349,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM CON-
OPERATING SYSTEM:
                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 38
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                 NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400
                            3 EKXXLXXXXXXXVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 EKXXLXXXXXXXVVXNA 19
                                                                                                                                                                                                                                                                                                              Haile, Lisa A.
                                                                                                                                                                                                                                         619/678-5099
                                                          Conservative
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29.4%;
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29.48;
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Pred. No. 6.6e+02,
2; Mismatches 10
                                                                        Score 20; DB 3;
Pred. No. 6.6e+02;
                                                          Mismatches
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                                                                                    Length 418;
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Search completed: February 28, 2002, 11:33:53 Job time: 29 sec

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Pred. No.
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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protein search,
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48
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## ALIGNMENTS

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A;Reference number: A82950; MUID:20437337
A;A;Accession: B83113 A, L. LUSS-reterences: EMBL:AL162875 A; Experimental source: cultivar Columbia; C; Genetics: R;Bevan, M.; Terryn, N.; Ardiles, ewes, H.W.; Rudd, S.; Lemcke, K.; submitted to the Protein Sequence A; Reference number: 224487
A; Accession: T48438 hypothetical protein T32M21.20 - Arabidopsis thallana (;Species: Arabidopsis thallana (mouse-ear cress) C;Species: Arabidopsis thallana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 C;Accession: T48438 RESULT T48438 C; Superfamily: catalase В 20 A; Experimental source: strain PAOI A;Cross-references: GB:AE004841; GB:AE004091; NID:g9950451; PIDN:AAG07624.1; GSPDB:GN A; Molecule type: DNA A; Residues: 1-482 <STO> A; Map position: 5 A; Introns: 37/3; 6 A; Molecule type: DNA A; Residues: 1-514 <BEV> A; Status: preliminary A;Status: preliminary Query Match Best Local S Matches 7 Genetics: Local Similarity 41.7 nes 7; Conservative katA; PA4236 N EEKTRLTTAAGAPVVDN 18 EEKXXLXXXXXXXVVXN 18 63/3; 107/3; 130/1; 150/3; 197/2; 239/3; 278/1; 307/3; 335/3; 442/3; 58.3%; 41.2%; 0,: Mayer, K.F.X. Database, March 2000 W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; Mayer, K.F.X. Score 28; I Pred. No. 2 A.L.; Mizoguchi, S.D.; Warrener, Coulter, S.N.; Folger, K.R.; Kas, Mismatches 15-Sep-2000 #text_change 31-Dec-2000 BAC clone T32M21 DB 2.7; 2; 10; Length 482; Indels 0 Caps Hickey, Larbig, 0

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A; Introns: 11/3;
                                                                                                                                                                                                                                                                                            R;Sammons, L.; Wohldmann, P.; Mullen, G. submitted to the EMBL Data Library, December 1997 A;Description: The sequence of C. elegans cosmid
                                                                                                                                                                                                                                                                                                                                                                                    C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T32767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler lebt, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, E.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanamoto, H.; Tepstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, Akuthors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Atitle: The complete genome sequence of the Gram-positive bacterium Bacillus subtills.
                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-408 < SAM>
                                                                                                                                                                                                                                               A; Description: The sequence A; Reference number: Z21222 A; Accession: T32767
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C; Superfamily: hypothetical protein
                                 A; Map position:
                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Experimental source: strain 168
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-214 <KUN>
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A;Accession: H69830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuar
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Nature 390, 249-256, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved hypothetical protein yhfK - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #tex
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                                                                                                        ;Cross-references: EMBL:AF039720; PIDN:AAB96696.1; GS;Experimental source: strain Bristol N2; clone F33D11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter, Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
                                                                                       Genetics:
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nes 7; Conser
                                                           CESP: F33D11.2
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5; Conserv
54/2; 193/3; 188/3; 268/3; 385/3
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29.4%;
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38
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Pred. No.
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12;
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18;
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                                                                                                                                    GSPDB:GN00019; CESP:F33D11.2
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probable fimbrial subunit protein PA0992 [imported] - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-205 <STO>
                                                                                                                                                                                                                                                                                adman, S.; Yuan, Y.; Brody, .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
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A81439
                                                                                                                                        C; Genetics:
                                                                                                                                                     A; Experimental
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                                                                                                                                                                                                                                                               A, Title: Complete genome
                                                                                                                                                                                                                                                                                                                              R;Stover, C.K.; Pham, X.Q.;
                                                                                                                                                                                                                                                                                                                                               C; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals A;Reference number: A81250; MUID:20150912
A;Accession: A81439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; V
                                                                                                                                                                      A; Cross-references:
                                                                                                                                                                                                                  A;Status:
                                                                                                                                                                                                                                                  A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AL139074; GB:AL1111168; NID:g6967505; PIDN:CAB72685.1; PID:g696
A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-113 <PAR>
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C; Species: Campylobacter
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                                         Similarity 6; Conserv
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6; Conser
                                                                                                                                                       source:
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                                         Conservative
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                                                                                                                                                       GB:AE004532; GB:AE004091;
ce: strain PAO1
                                                                                                                                                                                                                                                    A82950;
                                                                                                                                                                                                                                                  sequence of Pseudomonas aeruginosa 50; MUID:20437337
                                                        47.9%;
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                                                                                                                                                                                                                                                                                                                Erwin, A.L.; Mizoguchi, S.D.;
L.L.; Coulter, S.N.; Folger,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23; DB Pred. No. 19; 1; Mismatches
                                                        Score
Pred.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ced. No. 37;
Mismatches
                                           Mismatches
                                                        No.
                                                      ДВ
35;
                                                                                                                                                                    NID:g9946896; PIDN:AAG04381.1; GSPDB:GN
                                                                       2;
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                                                                       Length 205
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                                         Indels
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K.R.; Kas,
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6

KSILAAAVASLVVGNA

21

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phage lambda-related tail assembly protein G - Yersinia pestis plasmid pMT1 C:Species: Yersinia pestis
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 01-Dec-2000 C:Accession: T14970; T14644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R:Kaplan, N.; Johnson, D.; Schutz, K.; Gnoj, L.; Hoffman, J.; Till, S.; de la hl, M.; Martlenssen, R.; Chen, E.Y.; Wilson, R.; McComble, W.R. submitted to the EMBL Data Library, November 1998
A:Description: Sequence of A. thaliana BAC T10P11 from chromosome IV. A:Reference number: Z14248
A:Accession: T01078
                                               R:Lindler, L.E.; Plano, G.V.; Burland, V.; Mayhew, G.F.; Blattner, F.R. Infect. Immun. 66, 5731-5742, 1998
A;Title: Complete DNA sequence and detailed analysis of the Yersinia per A;Reference number: Z18268; MUID:99043898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein T10P11.2.2 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 24-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE005176; NID:g12723321; PIDN:AAK04541.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                В
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A; Introns: 35/1; 7:
A; Note: T10P11.2.2
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A;Accession: C86680
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A; Residues: 1-251 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prophage pil protein 08 [imported] - Lactococcus lactis subsp. lactis (strain C:Species: Lactococcus lactis subsp. lactis C:Species: Lactococcus lactis subsp. lactis c). Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
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Best Local Similarity 33...
6; Conservative
                                                                                                                                         ;Species: Yersinia pestis
;Date: 20-Sep-1999 #sequence_revision
;Accession: T14970; T14649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Residues: 1-1111 <KAP>
;Cross-references: EMBL:AC002330; NID:g2262135; PID:g3892059
;Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 6; Conserv
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Pred. No. 2.2e+02;
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Pred. No. 44;
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                                                                        Yersinia pestis
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                                                    RESULT
A86302
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hypothetical protein AAG10814.1
C; Species: Arabidopsis thaliana
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113 EKKIFISHSSKDKIVCNA

130

[imported] - Arabidopsis thaliana (mouse-ear cress)

2 EEKXXLXXXXXXXVVXNA 19

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A; Molecule type: DNA
A; Residues: 1-202 < LIN>
A; Residues: 1-202 < LIN>
A; Cross-references: EMBL: AF074611; NID: 93883003; PID: 93883053; PIDN: AAC82713.1
R; Hu, P.; Elliott, J.; McCready, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; submitted to the EMBL Data Library, March 1998
submitted to the EMBL Data Library, March 1998
A; Description: Structural organization of virulence determinants in three Yersi
                                                                                        C; Superfamily: Bacillus subtilis hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein yddK - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
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C;Superfamily: phage T4
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A; Accession: T14649
                                                                                                                                             A;Cross-references: GB:Z99106; GB:AL009126; NID:g2632653; PIDN:CAB12307.1; PID:g26328
A;Experimental source: strain 168
                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-266 <K
                                                                                                                                                                                                                                      A;Reference number: A69580; MUID:98044033
A;Accession: D69776
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A; Residues: 5-202 < HUP>
                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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                  Query Match
Best Local
                                                                                                                              Genetics
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                  45.8%;
27.8%;
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35.3%;
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                  Pred.
                                   Score 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 22;
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 Mismatches
                  No. 94;
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                                 DB 2;
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                                   Length 266;
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Indels
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Gaps
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R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID: 21016719
\C; Complex:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C:Accession: A86302 | R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.: White
                         A;Title: Crystal structure of Proteus mirabilis PR catalase with A;Reference number: A58664; MUID:95311317
A;Contents: annotation; X-ray crystallography, 2.2 angstroms
                                                                                                     A;Contents: annotation; X-ray crystallography, A;Note: native Fe(III) with NADPH R;Gouet, P; Jouve, H.M.; Dideberg, O. J. Mol. Biol. 249, 933-954, 1995
                                                                                                                                                                                                                                          R;Gouet, P.; Jouve, H.M.; Dideberg, O. submitted to the Brookhaven Protein Data
                                                                                                                                                                                                                                                                                             A; Contents: annotation; X-ray crystallograph A; Note: compound II, dithiothreitol reduced
                                                                                                                                                                                                                                                                                                                                                   submitted to the Brookhaven Protein Data Bank, June 1996 A; Reference number: A67901; PDB:2CAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the Brookhaven Protein Data Bank, A; Reference number: A67900; PDB:2CAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A67899; PDB:2CAE
A; Contents: annotation; X-ray crystallography,
R; Gouet, P.; Jouve, H.M.; Hajdu, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Gouet, P.; Jouve, H.M.; Dideberg, O. submitted to the Brookhaven Protein Data Bank, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Variety: strain Pr, peroxide resistant
C;Date: 19-Nov-1997 #sequence_revision 21-Nov-1997 #text_change 15-Sep-2000
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                                                                                                                                                                                                                    A; Reference number: A67902; PDB: 2CAH
                                                                                                                                                                                                                                                                                                                                                                                                              R;Gouet,
                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Contents: annotation; A; Note: compound I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Buzy, A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  catalase (EC 1.11.1.6) [validated] - Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-387 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Accession: A58663; B58663; Buzy, A.; Bracchi, V!; St. Protein Chem. 14, 59-72,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: B58663
Molecule type: DNA
Residues: 1-305,'AE' <BUZ2>
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Best Local Similarity
Matches 5; Conser
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Map position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12
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                                                                                                                                                                                                                                                                                                                                                                                                              P.; Jouve, H.M.; Hajdu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDKSSTKPASSSTVVSN 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                            X-ray crystallography, 2.7 angstroms,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-ray crystallography, 2.7 angstroms,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sterjiades, R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.8%;
29.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 22; DB 2;
Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                             Bank, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chroboczek, J.; Thibault, P.;
                                                                                                                                                                                                                                                                                                   compound
                                                                                                                                                                                       2.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.2 angstroms,
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C; Function:

A; Description: Catalyzes the conversion of two of molecules of hydrogen A; Note: this enzyme has a tightly bound NADPH cofactor

A; Note: this enzyme has a tightly bound NADPH cofactor

C; Superfamily: Catalase

C; Superfamily: Catalase

C; Seywords: Chromoprotein; heme; homotetramer; iron; metalloprotein; NAI

F; 53/Modified site: methionine sulfone (Met) #status experimental

F; 54,93,127/Active site: His, Ser, Asn #status predicted

F; 337/Binding site: heme iron (Tyr) (axial ligand) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F42G9.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #t. C;Accession: T16334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
T16354
                                                                                                                                                                                                                                             hypothetical protein [imported] - Lactococcus lactis subsp. lactis C:Species: Lactococcus lactis subsp. lactis C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-C:Date: 23-E86787
                                                                                                                                                                                                                                                                                                                                   E86787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: CESP: F42G9.1
A; Introns: 37/3; 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, March A;Description: The sequence of C. elegans A;Reference number: Z18498
                    A;Cross-references: GB:AE005176; NID:g12724279; PIDN:AAK05399.1; GSPDB:GN00146
A;Experimental source: strain IL1403
                                                                   A; Molecule type: DNA
A; Residues: 1-653 <STO>
                                                                                                               A; Status: preliminary
                                                                                                                                    A; Reference number: A; Accession: E86787
                                                                                                                                                         A;Title: The complete genome sequence of the lactic acid bacterium A;Reference number: A86625 \,
                                                                                                                                                                                                        Genome Res. in press, 2001
                                                                                                                                                                                                                          R; Bolotin, A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-491 <TAI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A; Accession: T16354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Taich,
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Best Local S
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Genetics:
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6; Conservative
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6; Conservative
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ce: strain Bristol N2
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                                                                                                                                                                                                                            P.; Mauger, S.; Jaillon, O.;
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1.8e+02;
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Conservative

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45.8%; 29.4%;

Score 22; DB 2; Pred. No. 2.5e+02 Mismatches

Length 653

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C:Accession: H70024; E54078

C:Accession: H70024; E54078

C:Accession: H70024; E54078

C: Bron, S: Brouillet, S:; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A: Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
Authors: Schleich, S.; Schroetter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
euchl, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
J.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A; Reference number: A69580; MUID:98044033
A; Accession: H70024
A. Status, T. Status, T. Scoffone, Translation not shown
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
Search completed: February 28, 2002, 11:35:08 Job time: 104 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;HAnlon, D.W.; Ordal, G.W.
J. Biol. Chem. 269, 14038-14046, 1994
A;Title: Cloning and characterization of genes encoding methyl-accepting chemotaxis prot
A;Reference number: A54078; MUID:94245722
A;Accession: E54078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: short-chain alcohol dehydrogenase homology <SADH>
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A; Residues: 1-689 <KUN>
A; Residues: 1-689 <KUN>
A; Cross-references: GB: Z99119; GB: Z99120; GB: AL009126; NID: g2635613; PIDN: CAB15111.1; PI
A; Experimental source: strain 168
R; Hanlon, D.W.; Ordal, G.W.
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A; Residues: 1-31 <HAN>
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Best Local Similarity 35.:
Matches 6; Conservative
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35.3%;
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Pred. No. 2.6e+02;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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 protein search, using sw model
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CATA_PROMI
P2C1_CAEEL
YUXG_BACSU
POLA_ETON
GSA_LYCES
GYRB_BARBA
YC31_SCHPO
POLR_TYMV
POLR_TYMV
POLR_TYMV
POLR_TYMV
POLR_TYMV
R17_STAAU
RS2_SULAC
STPA_STAAU
RNC_MYCTU
GLPR_ECOLI
E2BA_HUMAN
RLX3_STAAU
YDGC_SCHPO
SHL_BRARE
MENF_BACSU
GSA_TOABC
GT71_CAEEL
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p10358 turnip yell
p20128 turnip yell
p20475 turnip yell
p29475 streptomyce
o51142 borrelia bu
p44020 haemophilus
p39478 sulfolobus
p319478 sulfolobus
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p319478 sulfolobus
p319478 staphylococ
Q10962 mycobacteri
O51391 pseudomonas
046813 escherichia
Q14232 homo sapien
p14491 staphylococ
Q10498 schizosacch
Q92008 brachydanio
p23973 bacillus su
p31593 nicotiana t
Q11085 caenorhabdi
Q00336 saccharomyc
Q92244 homo sapien
p53354 aedes aegyp
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                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed.
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BINDING
SEQUENCE
                                                                                                                                 Membrane.
                                                                                                                                         EMBL; AJ011680; CAB53860.1;
                                                                                                                                                                                                                                                                                    TISSUE=Mammary gland;
Nielsen R.L., Andersen M.H.,
                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoė; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovinae; Bosinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                    20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ADIPOPHILIN (ADIPOSE DIFFERENTIATION-RELATED PROTEIN) (ADRP).
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ACT_SITE
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20-AUG-2001
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ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
                                                                                                                                                                                                                                                                              Petersen T.E.;
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38.9%;
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Pred. No.
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Pred. No.
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BY SIMILARITY.
PROXIMAL HEME LIGAND (BY SIMILARITY).
84E5ABA647CAB414 CRC64;
  PRT;
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Mismatches
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RESULT 4
CATA_PROMI
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Best Local :
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P42321;
01-NOV-1995 (
01-NOV-1995 (
01-NOV-1997 (
                                                                                                    Gagnon J., Jouve H.-M., Hudry-Clergeon G.;
"Complete amino acid sequence of Proteus mirabilis PR catalase. Occurrence of a methionine sulfone in the close productive site.";
MEDLINE=95311317;
Gouet P., Jouve H
                                      STRAIN-PR;
                                                                                                                                                                                                                                                                                                                                      KATA.
                                                                                                                                                                                                               STRAIN-PR;
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                                                   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                                                                                                                                                                                              SEQUENCE, AND SEQUENCE OF 1-305 FROM N.A
                                                                                                                                                                                                                                                               NCBI_TaxID=584;
                                                                                                                                                                                                                                                                                   Proteus
                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                     Proteus mirabilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institute. There are no rest modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.in-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X97324; CAA65989.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Adipocyte differentiation-related protein is constituent of milk lipid globule membrane."; Biochem. J. 320:1025-1030(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97157014; PubMed=9003395; Heid H.W., Schnolzer M., Keenan T.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Mammalia; Eutheria;
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20-AUG-2001
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30-MAY-2000
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-1- PIM: ACYLATED; PRIMARILY WITH C14, C16 AND C18
-1- SIMILARITY: BELONGS TO THE PERIPILIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity hes 5; Conserv
                                                                                     Protein Chem. 14:59-72(1995).
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437 AA; 48100 MW;
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(Rel. 32, Last sequence up
(Rel. 35, Last annotation
C 1.11.1.6).
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   H.-M.,
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                  PubMed=7791219;
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J. Mol. Biol. 249:933-954
-i- FUNCTION: DECOMPOSES
                                                                                                                                            Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
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PDB; 2CAF; 07-DEC-96.
PDB; 2CAG; 07-DEC-96.
PDB; 2CAG; 11-JAN-97.
InterPro; IPR002226; Catalase.
                                                                                                                          This
                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
01-CCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PROBABLE PROTEIN PHOSPHATASE 2C F42G9.1 (EC 3.1.3.16) (PP2C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oxidoreductase;
          EMBL: U00051;
HSSP: P35813;
                                                or send an email to license@isb-sib.ch).
                                                           entities
                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as iong as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                            STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Rhabditidae; Pelodei
                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                     F42G9.1.
                                                                                                                                                                                                                                                                                                                                                                                   P2C1_CAEEL P49595;
                                                                                                                                                                                                                                                                                                                                                                                                             CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3D-structure.
                                                                                                              between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: HOMOTETRAMER.
SUBCELLULAR LOCATION: CYTOPLASMIC.
SUBCELLULAR LOCATION: CYTOPLASMIC.
MASS SPECTROMETRY: MW-55643; MW_ERR-5; METHOD-ELECTROSPRAY
SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN CATALYTIC ACTIVITY: 2 H(2)0(2) = O(2) + 2 H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COFACTOR: HEME GROUP AND NADP.
                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKXXLXXXXXXXVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKKKLTTAAGAPVVDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 37.5
6; Conservative
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54
127
                                                                                                                                                                                                                                                                                Peloderinae;
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             1A60
                      AAA91358.1;
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                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peroxidase;
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55614 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of Proteus mirabilis PR catalase with and without
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54
127
                                                                                                                                                                                                                                                                                Nematoda; Chromadorea;
Inae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Iron; Heme; Hydrogen peroxide; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 22; DB Pred. No. 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROXIMAL HEME LIGAND.
ADC25F3CB41F5C50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METHIONINE SULFONE
                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 491
                                                                                    There are no restrictions ong as its content is in
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                                                                                                                                                                                                                                                                                              Rhabditida; Rhabditoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 484;
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PEROXIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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RESULT 6
YUXG_BACSU
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Best Local S
Matches 6
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METAL
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InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL OXIDOREDUCTASE IN GBSA-TLPB INTERGENIC REGION
(EC 1.-.-.) (ORF2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00332; PP2Cc; 1.
SMART; SM00331; PP2C_SIG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00481; PP2C;
                                                                                   EMBL; 293938; CAB07952.1; -.
EMBL; L29189; AAA2058.2; -.
EMBL; 293119; CAB15100.1; -.
EMBL; 299120; CAB15111.1; -.
EMBL; 299120; CAB15111.1; -.
EMBL; P25529; IAHI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hanlon D.W., Ordal G.W.; "Cloning and characterization of genes encoding methyl-accepting chemotaxis proteins in Bacillus subtilis.";
J. Biol. Chem. 269:14038-14046(1994).
-:- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=168 / OI1085;
MEDLINE=94245722; Pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus subtilis.
Bacteria; Firmicutes; Bacteria; Firmicutes; Bacillus/Staphylococcus
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01032; PP2C; 1
                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oudega B., Koningsteyn
Submitted (APR-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P40747;
                 HSSP, P25529; 1AHI.
Subtilist; BG10947; yuxG.
InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-49 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YUXG OR YULA
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                                                                                                                                                                                                                                                                                                                                                                                                                               (SDR) FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR003589; PP2C_cata
IPR001932; PP2C_doma
IPR003588; PP2C_sig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR000222; PP2C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 protein; Hydrolase; MANGA
37 37 MANGA
38 MANGA
57 57 MANGA
428 428 MANGA
477 477 MANGA
491 AA; 53141 MW; F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    491 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=8188684;
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33,3%;
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the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Olase; Magnesium; Manganese.

MANGANESE 1 (BY SIMILARITY).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 1 AND 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feger G., Pohl T.;
e EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>,,</u>
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Pred. No. 1e+0
1; Mismatches
                                                                                                                                                                                                                                                                                     is not removed.
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1e+02;
                                                                                                                                                                                                                                                                                                              as its content
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                                                                                                                                                                                                                                                                 http://www
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                       Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               databases
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RESULT 7
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SQ
           Pfam; PF00548; Cys-protease-3C; 1. Pfam; PF02226; Pico_PlA; 1. Pfam; PF00947; Pico_P2A; 1. Pfam; PF00547; Pico_P2B; 1. Pfam; PF00073; rhv; 3. Pfam; PF00680; RNA_dep_RNA_pol; 1. Pfam; PF00910; RNA_helicase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                  InterPro; IPR000199; Cys-protease-3C.
InterPro; IPR003138; Pico_PlA.
InterPro; IPR00081; Pico_P2A.
InterPro; IPR002527; Pico_P2B.
InterPro; IPR000605; RNA_helicase.
InterPro; IPR001205; RNA_pol_P3D.
InterPro; IPR001676; RNA_pol_P3D.
InterPro; IPR001676; RNA_pol_P3D.
                                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete nucleotide sequence of enterovirus type 70: relationships with other members of the picornaviridae.";
J. Gen. Virol. 71;2291-2299(1990).
-i- FUNCTION: P3C, POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERT Q/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.
-i- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNIT EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical
ACT_SITE 5
SEQUENCE 68
                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                           PIR; A36253;
HSSP; P03299;
                                                                                                                                                                                                                                                                                          EMBL; D00820;
                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ryan M.D., Jenkins O., Hughes P.J., Minor P.D., Almond J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91037960; PubMed=2172447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1993 (Rel. 27, Created)
01-NOT-1995 (Rel. 32, Last sequence update)
01-NOT-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS P2A TO P2C, P3A; GENOME-LINKED PROTEIN VPG; PICORNAIN 3C
(EC 3.4.22.28) (P3C); RNA-DIRECTED RNA POLYMERASE P3D
(EC 2.7.7.48)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human enterovirus 70 (strain J670/71) (EV 70) Viruses; ssRNA positive-strand viruses, no DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=31915;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       VP3, AND VP4.
PTM: SPECIFIC ENZYMATIC OF SIMILARITY: THE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                               European
                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a case the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                               C03.020;
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6; Conser
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579 579
689 AÅ; 76020 MW;
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                                                                                                                                                                                                                                                                                                                                                              Bioinformatics Institute. The profit institutions as long
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35.3%;
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9 BY SIMILARITY.
6020 MW; 88A82FDC3EEDDOFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     CLEAVAGES IN VIVO YIELD MATURE F
E BELONGS TO PEPTIDASE FAMILY C3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 22; DB
Pred. No. 1.4e
1; Mismatches
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1.4e+02;
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                                                                                                                                                                                                                                                                                                                                               Usage
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                                                                                                                                                                                                                                                                                                                                                                            restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Picornaviridae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEINS
                                                                                                                                                                                                                                                                                                                                              for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNITS,
VP1, VP2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Booth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                            collaboration -
                                                                                                                                                                                                                                                                                                                                                                                         outstation
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RESULT 8
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Best Local S
Matches 6
                                                                               between
the Euro
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01-NOV-1995
20-AUG-2001
                                                                                                                                                                                                               SEQUENCE FROM N.A.

STRAIN-ED / KW20 / ATCC 51907;

MEDLINE-95350630; PubMed-7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Heblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIPID
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                      Science
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CHAIN
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                                                                                                                                                                                                          Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                       Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polyprotein;
RNA-directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD001274; Pico_P2B; ProDom; PD001306; Pico_P2A;
                                                                                                                                                                                          Whole-genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                (POTENTIAL).
SIMILARITY:
                                                                                                                                                          SUBCELLULAR LOCATION:
U32766;
HI0850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEKGTLYTSPFLIATTNA 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEKXXLXXXXXXXVVXNA
                                                                                                                                                                     269:496-512(1995).
                                                       non-profit institutions as long and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                    Proteobacteria; gamma subdivision; Pasteurellaceae;
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(Rel.
(Rel.
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RNA p
          AAC22507.1;
                                                                                                                                                                                          random sequencing
                                                                                                                                  TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
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                                                                                                                                                       INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
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COAT PROTEIN VP2 (P1B).

COAT PROTEIN VP3 (P1C).

COAT PROTEIN VP3 (P1C).

COAT PROTEIN VP3 (P1D).

COAT PROTEIN P2A.

CORE PROTEIN P2B.

CORE PROTEIN P2C.

CORE PROTEIN P3A.

CORE PROTEIN P3A.

GENOME-LINKED PROTEIN VPG (P3B).

PICORNAIN 3C.

RNA-DIRECTED RNA POLYMERASE P3D.

MYRISTATE (BY SIMILARITY).
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Pred.
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PROTEASE (POTENTIAL).
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No.
                                                                                                                                                                                         assembly of Haemophilus
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                                                                 There are no rest
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(P1A).
(P1B).
(P1C).
(P1D).
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SPER

Hypothetical I TRANSMEM 11 TRANSMEM 11 SEQUENCE 14

105 144 AA;

125 I 15841 MW;

POTENTIAL

564FC10BDE2CA4BD

CRC64;

protein; Transmembrane; Cc 76 96 POTENTIAL.

Complete

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Best Local
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GSA_LYCES STANDARD; PRT; 481 AA.

Q40147;

Q1-NOV-1997 (Rel. 35, Created)

Q1-NOV-1997 (Rel. 35, Last sequence update)

15-JUL-1998 (Rel. 36, Last sequence update)

GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (EC

GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (EC

GLUTAMATE-1-SEMIALDEHYDE AMINOTENSFERASE) (GSA-AT).
                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN-CV. VENT CHERRY; TISSUE-Fruit;

STRAIN-CV. VENT CHERRY; TISSUE-Fruit;

POIKing G.F., Hannapel D.J., Gladon R.J.;

A cDNA clone for glutamate 1-semialdehyde 2,1-aminomutase

"A CNTALYTIC ACTIVITY: (S) 4-AMINO-5-OXOPENTANOATE -

"S-AMINOLEVULINATE.

"S-AMINOLEVULINATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lycopersicon esculentum (Tomato).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                    BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L39279; AAA81881.1; -. HSSP; P24630; 3GSA.
                                                                                                                                                                                                                                                                                                                                                                                                              PROSTTE: PS00600; AA_TRANSFER_CLASS_3; 1.
PROSTTE: PS00600; AA_TRANSFER_CLASS_3; 1.
Porphyrin blosynthesis; Chlorophyll blosynthesis; Isomerase;
Pyridoxal phosphate; Transit peptide; Chloroplast.
Pyridoxal phosphate; Transit peptide; Chloroplast.
TRANSIT 1
Prostrement 1
TRANSIT 1
Prostrement 1
P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR000954; Aminotran_3.
Pfam; PF00202; aminotran_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71
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        N
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SUBCELLULAR LOCATION: CHLOROPLAST.
SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COFACTOR: PYRIDOXAL PHOSPHATE PATHWAY: SECOND STEP IN PORPH
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6; Conser
                                                                               6; Conserv
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                                                                                                                                                                                                                                                                                    321
481 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECOND STEP IN PORPHYRIN BIOSYNTHESIS IN CHLOROPHYLL BIOSYNTHESIS.
                                                                                        Conservative
                                                                                                                                                                                                                                                                                        481
321
51413
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                                                                                                                             33.38;
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Pred. No.
                                                                                            Score 21; DB Pred. No. 1.9e.
                                                                                                                                                                                                                                                                                    GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PYRIDOXAL PHOSPHATE (BY SIMILARITY).
4D7EFC0E32D64BBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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57;
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Query Match Best Local S Matches 5

Similarity 5; Conserv

Conservative

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43.8%;

Score 21; DB 1; Pred. No. 2.8e+02; Mismatches

Length 692

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Gaps

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RESULT
GYRB_BA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
Bartonellaceae; Bartonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BARBA
                                                                                                                                                                                                                                                                                                                                                                                                  Topoisomerase; Isomerase; F
VARIANT 124 124
VARIANT 184 184
VARIANT 214 214
VARIANT 214 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99013570; PubMed-a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Battisti J.M., Smitherman L.S., Samuels D.S. "Mutations in Bartonella bacilliformis gyrB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYRB.
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                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=774;
VARIANT
VARIANT
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SEQUENCE
                                                                        PRINTS; PRO0418; TPIZFAMILY.

ProDom; PD000616; DNA_topoisoI; 1.

ProDom; PD149633; DNA_gyraseB_C; 1.

SMART; SM00387; HATPase_C; 1.

SMART; SM00433; TOP2C; 1.

PROSITE; PS00177; TOPOISOMERASE_II;
                                                                                                                                           pfam; pF00986; DNA_gyraseB_C; pfam; pF00204; DNA_topoisoII; pfam; pF02518; HATPase_C; 1. pfam; pF01751; Toprim; 1.
                                                                                                                                                                                           Interpro: IPR000410; Bctrl_sensor.
Interpro: IPR002288; DNA_gyraseB_C.
Interpro: IPR0012141; DNA_topoisoII.
Interpro: IPR0013594; HATPase_C.
Interpro: IPR002936; Toprim.
                                                                                                                                                                                                                                                         EMBL; U82225; AAC71079.1;
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SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
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   ÀΑ;
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184
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  e; ATP-binding; Antiblotic resist
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T -> A (IN COUMERMYCIN A1 M
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T -> F54948EEF342281F CRC64;
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SMART; SM00239; C2; 3.

PROSITE; PS50004; C2_DMAIN_2;
                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                    Hypothetical protein;
TRANSMEM 197 217
TRANSMEM 225 249
TRANSMEM 744 841
                                                                                                                                                                                                                                                                                                     EMBL; AL121859; CAB58375.1; -.
EMBL; AL031333; CAA20433.1; -.
EMBL; D89235; BAA13986.1; ALT_I
HSSP; P04410; 1A25.
                                                           135 EKQDLQSALPSDAVSNA 151
                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YOShioka S., Kato K., Okayama H.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.

-I- SIMILARITY: CONTAINS 2 C2 DOMAINS.

-I- CAUTION: REF 2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
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Submitted (AUG-1998)
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                                                                                                                                                                                                                                                                                         nterPro; IPR000008; C2.
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Wedler H., Duesterhoeft A., McDougall R.C., Rajandream M.A.,
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=972;
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                                                                                      3 EKXXLXXXXXXXVVXNA 19
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  STANDARD;
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245
841
1161
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                                                                                                                                                                           156031 MW;
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scomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                    Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to the EMBL/GenBank/DDBJ databases
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                                                                                                         Score 21; DB 1; pred. No. 5.8e+02; marches 11;
                                                                                                                                                                   POTENTIAL.
POTENTIAL.
C2 DOMAIN 1
C2 DOMAIN 2.
MW; 617A91286ALFBCC6 CRC64;
 PRT;
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1776 AA
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l IN CHROMOSOME III.
                                                                                                                                  Length 1429;
                                                                                                           Indels
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Query Match
Best Local S
Matches 5
                                                           use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                   "Overlapping open reading frames revealed by complete nucleotide sequencing of turnip yellow mosaic virus genomic RNA."; nucleic Acids Res. 16:6157-6173(1988).

-!- MISCELLANEOUS: THE 206 KDA PROTEIN IS POTENTIALLY A POLYPROTEIN (BY HOMOLOGY TO THE LONGER PROTEIN OF THE SINDBIS VIRUS).
                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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EMBL; X07441; CAA30322.1; PIR; S01956; S01956.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _TYMV
                                                                                                                                                                                                                                                                                                                                                                                               Morch M.D., Boyer J.C., Haenni A.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=88289359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Turnip yellow mosaic virus.
Viruses; ssRNA positive-str
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Pfam; PF01443; Viral_helicasel; 1.

Pfam; PF01443; Viral_helicasel; 1.

Transferase; RNA-directed RNA polymerase; Polyprotein; ATP-binding.

NP_BIND 899 906 ATP (BY SIMILARITY).

SEQUENCE 1776 AA; 198127 MW; 1C2E37B9EC3A5333 CRC64;
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01-FEB-1991
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MEDLINE-90021186; PubMed-2800337;

Ding S.W., Keese P., Gibbs A.;

"Nucleotide sequence of the ononis yellow mosaic tymovirus genome.";

"Virology 172:555-563(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J04375; AAA46796.1; -.
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01-FEB-1991 (Rel. 17, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat
RNA REPLICASE POLYPROTEIN (EC 2.7.7.48).
Ononis yellow mosaic virus.
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POLR_TYMVC
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Pfam; PF01443; Viral_helcasel; 1.

Transferase; RNA-directed RNA polymerase; Polyprotein; ATP-binding.

NP_BIND 976 983 ATP (BY SIMILARITY).

DOMAIN 1631 1665 POLYMERASE SITE (BY SIMILARITY).

SEQUENCE 1844 AA; 206510 MW; CB447EF05F199A18 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDITINE-90021184; PubMed-2800335;
MEDETINE-90021184; PubMed-2800335;
Medese P., Mackenzie A., Gibbs A.;
Nucleotide sequence of the genome of an Australian isolate of turnip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLR_TYMVA STANDARD; PRT; 1844 AA.
P20128;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RNA REPLICASE POLYPROTEIN (EC 2.7.7.48)
Turnip yellow mosaic virus (Australian isolate).
Viruses; ssRNA positive-strand viruses, no DNA stage; Tymovirus
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                                                  POLR_TYMVC P28477;
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Transferase;
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Pro; IPRO0606; Viral_helcsel.
PF01443; Viral_helicasel; 1.
PF01443; Viral_helicasel; 1.
PF01443; Viral_helicasel; 1.
PF01443; Viral_helcsel.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
NN 1631 1665 POLYMERASE SITE (BY SIMILARITY).
PNCE 1844 AA; 206640 MW; A016D75BCB3D12BC CRC64;
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5; Conservative
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                                                                 STANDARD;
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Pred. No. 7.6e+02;
1; Mismatches 11;
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Best Local
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Pfam; Pf01443; Viral_hellcasel; 1.
Transferase; RNA-directed RNA polymerase; Polyprotein; ATP-binding.
NP_BIND 976 983 ATP (BY SIMILARITY).
DOMAIN 1631 1665 POLYMERASE SITE (BY SIMILARITY).
SEQUENCE 1844 AA; 206612 MW; O2CB928FCCCA5EA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genomic RNA sequence of turnip yellow mosaic virus isolate TYMC, a CDNA-based clone with verified infectivity."; plant Mol. Biol. 18:403-406(1992).

-i- MISCELLANEOUS: THE 206 KDA PROTEIN IS POTENTIALLY A POLYPROTEIN (BY HOMOLOGY TO THE LONGER PROTEIN OF THE SINDBIS VIRUS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-92119261; PubMed-1731998;
Dreher T.W., Bransom K.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA REPLICASE POLYPROTEIN (EC 2.7.7.48).
Turnip yellow mosaic virus (isolate TYMC).
Viruse; ssRNA positive-strand viruses, no DNA stage; Tymovirus.
NCBI_TaxID=31751;
[1]
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29.4%;
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Pred. No. 7.6e+0
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## ALIGNMENTS

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Best Local :
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BU Arabidopsis sequencing project;
BU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AL162875; CAB85548.1; -.

InterPro; IPR001798; Kelch.
Pfam; PF01344; Kelch; 3.

Hypothetical protein.

SEQUENCE 514 AA; 56659 MW; D362EB63687B984D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9LZ83 PRELIMINARY; PRT; 314 MA. Q9LZ83; Q9LZ83; COT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) HYPOTHETICAL 56.7 KDA PROTEIN.
                                                                                                                                                                                                                                                                       Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villarcel R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
      407
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[1]
                                                                 Local Similarity nes 7; Conserv
                                 2 EEKXXLXXXXXXXVVXNA 19
EEKRALESSIAETQVENA 424
                                                             Conservative
                                                                           54.2%;
38.9%;
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Pred. No.
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0; Mismatches
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
ADIPOCYTE DIFFERENTIATION-RELATED PROTEIN (FRAGMENTS).
Bos taurus (Bovine)
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Heid H.W., Schnolzer M., Keenan T.W.;
Padipocyte differentiation-related protein
constituent of milk lipid globule membrane.
Biochem. J. 320:1025-1030(1996).
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Mammalia; Eutheria; Cetartiodactyla;
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                                                                                                                                                                                                                                                                                                      "Isolation and characterization of a partial cDNA coding adipose differentiation related protein."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF234676; AAF76320.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9MZE5;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
ADIPOSE DIFFERENTIATION-RELATED PROTEIN (FRAGMENT).
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos.
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27
34
54
84
100
108
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                                                                                                                                  vative
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                                                                                                                                                                                                                                                                                            44491 MW;
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                                                                                                                                                                52.1%;
38.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25; DB Pred. No. 14; 1; Mismatches
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                                                                                                                                     ۲
                                                                                                                                                                    Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                6764A09E262CD673 CRC64;
                                                                                                                                         Mismatches
                                                                                                                                                                    25;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                     Length 404;
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Sus.
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Q9H5Z1
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Best Local S
Matches 6
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DJ616B8.1 (SIMILAR TO PRE-MRNA SPLICING RNA HELICASE)
DJ616B8.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9H4H7
Q9H4H7;
                                                                                                                                                                                                                           Obayashi M., Nishi T., Shibah Isogai T., Sugano S.;
"NEDO human cDNA sequencing p submitted (AUG-2000) to the E -i- SIMILARITY: TO HELICASE C EMBL; AKO26412; BABL5476.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2001) to the EMBL - SIMILARITY: TO HELICASE C-TE EMBL; ALO23803; CACO3449.3; - IPRO01410; DEAD InterPro; IPRO01650; Helicase_C. InterPro; IPRO01650; Helicase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9H5Z1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00271; helicase_C; SMART; SM00487; DEXDC; 1. SMART; SM00490; HELICC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TYEMBLEE). 16, Created)
01-MAR-2001 (TYEMBLEE). 16, Last sequence up
01-JUN-2001 (TYEMBLEE). 17, Last annotation
CDNA: FLJ22759 FIS, CLONE KAIA0875.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP-binding; Helicase.
                                                                                                 Interpro; IPR001410; DEAD.
Interpro; IPR001650; Helicase_C.
pfam; PF00271; helicase_C; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
                                                                                                                                                                                                                                                                                                                                                    Kawakami T., Noguchi S., Itoh T., Shi
Nakajima Y., Mizuno T., Morinaga M.,
Yamada K., Fujii Y., Ozaki K., Hirao
Obayashi M., Nishi T., Shibahara T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-ILEAL MUCOSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia;
                                                        SMAKI; SMAKU;
ATP-binding; Helicase.
703 AA; 78811 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40
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                                                                                                                                                                                                                                                                                                                                                            Itoh T., Shigeta K., Senba T., Matsumura K.,
Morinaga M., Tanigami A., Fujiwara T., Ono T.,
ki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,
hibahara T., Tanaka T., Nakamura Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ databases C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                          project.";
EMBL/GenBank/DDBJ databases
C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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Pred.
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7A2E8DE2F7197746 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                   CFC94B3F90CE580C CRC64;
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
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Length 703
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Query Match

52.1%;

Score

25;

DВ

4;

Best Local Matches

Similarity 35.3 6; Conservative

35.3%;

Pred. No. 79; 1; Mismatches

10;

Indels

0,

Gaps

0;

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RX MEDLINE-98044033; PubMed-9384377;
RX MEDLINE-98044033; PubMed-9384377;
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Bignell S.C.,
RA Borriss R., Boursier L., Brans A., Braun M., Bignell S.C.,
RA Broulllet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devlne K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Chims S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Ghims S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Gliseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Kurita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Noone D., O'Reilly M., Ogawa K., Ogivara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Perescott A.M.,
RA Parro V., Forting C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Seto T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Setiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Setiguchi M., Tanckoshi A., Tanaka T., Tarkanaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Viania A., Waller E., Wedler E., Wedler F., Vasanct K.,
RA Winters P., Wipta A., Yanamoto H., Yamane K., Yasamoto K., Yata K.,
RYOShida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT The complete genome sequence of the gram-positive bacterium Baciilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
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01-JUL-1997
01-JUL-1997
01-NOV-1998
                                Kunst F., Ogasawara N., Yoshikawa H., Submitted (NOV-1997) to the EMBL/GenBa EMBL; Y14083; CAA74532.1; -EMBL; 299109; CAB12866.1; -.
     Hypothetical protein; SEQUENCE 214 AA; 2
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Submitted (JUN-1997) t
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                                                                                                               STRAIN-168
                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                              Nature 390:249-256(1997).
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Matches
STRAIN-BRITOL NZ:
STRAIN-BRITOL NZ:
Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson /
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
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SEQUENCE
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01-MAY-1999
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BTL-II (MHC
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01-JUN-1998 (TrEMBLrel.
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F33D11.2 PROTEIN.
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098261;
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Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caer
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InterPro;
                                                                                                                SEQUENCE FROM N.A
                                                                                                                                      NCBI_TaxID=6239;
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Mammalia; Eutheria;
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5; Conservative
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IPR003006;
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Primates;
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NOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                 oda; Chromadorea; Caenorhabditis.
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ATED BUTYROPHILIN-LIKE) (FRAGMENT).
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                                                                                                                                                                                                                                                    PRT;
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Waterston R.,

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                                         O9UIRO PRELIMINARY;
O9UIRO;
01-MAY-2000 (TIEMBLIEL 1
01-MAY-2000 (TIEMBLIEL 1
01-JUN-2001 (TIEMBLIEL 1
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01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-20002427; Pubmed-10529413; MEDLINE-20002427; Pubmed-10529413; Chan A.P., Kloc M., Etkin L.D.; "fatvg encodes a new localized RNA that us (FVLE1) to localize to the vegetal cortex Development 126:4943-4953(1999).

EMBL; AF184090; AAF1961111; -
                                                                                                                                                                                                                                                                                                                                                                                                                FATVG.
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                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; l
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston
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                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                    Xenopodinae; Xenopus
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  Eukaryota;
              Homo sapiens
                                    BUTYROPHILIN-LIKE
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AF039720; AAB96696.1; -.
NCE 408 AA; 45741 MW;
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6; Conser
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   Metazoa;
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              (Human)
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tock L., Wilkinson-Sproat J., Wohldman
guous nucleotide sequence from chromosc
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    Chordata;
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13,
17,
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    Craniata;
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    Vertebrata;
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    Euteleostomi;
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STRAIN=NCTC 11168;
MEDLINE=20150912; PubMed=10688204;
MEDLINE=20150912; PubMed=10688204;
MEDLINE=20150912; PubMed=10688204;
MEDLINE=20150912; PubMed=10688204;
Markhill J., Wren B.W., Mungall K., Ketley J.M.
Basham D., Chillingworth T., Davies R.M., Felt
Jagels K., Karlyshev A.V., Moule S., Pallen M..
Jagels K., Karlyshev A.V., Mutherford K.M., V.
Quail M.A., Rajandream M.A., Rutherford K.M., V.
Whitehead S., Barrell B.G.;
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathoge:
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01-OCT-2000
01-OCT-2000
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01-OCT-2000 (TrembLrel. 15, I
01-MAR-2001 (TrembLrel. 16, I
HYPOTHETICAL PROTEIN CJ0202C:
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SMART; SM00409; IG; 2.
SMART; SM00410; IG_11ke; 1
SEQUENCE 455 AA; 50436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stammers M., Rowen L., Rhodes D., Trowsdale J., Beck S.; "Characterization of BTL-II: A polymorphic butyrophilin-like located at the border of the MHC class II and class III regions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Primates; Catarrhini;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CJ0202C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9PIS7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003599; Ig.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                Hypothetical protein; Complete SEQUENCE 113 AA; 12679 MW;
                                                                                                                                                                                                                                     reveals hypervariable sequences.";
Nature 403:665-668(2000).
EMBL; AL139074; CAB72885.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campylobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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AF186590;
EEKTFVSDKITQVVAENA
                                           EEKXXLXXXXXXXVVXNA
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AF186588; AAF05530.1;
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6; Conservative
                                                                                    Similarity 6; Conserv
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AAF05530.1;
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Pred. No. 1e+(
2; Mismatches
                                                                                       Score 23; DB Pred. No. 45; 1; Mismatches
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R.M., Feltwell
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1e+02;
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ell T., Holroyd S
., Penn C.W.,
an Vliet A.H.M.,
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Matches 6
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Best Local S
Matches 6
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01-JUN-2001 (TrEMBLrel. 17, C
01-JUN-2001 (TrEMBLrel. 17, I
01-JUN-2001 (TrEMBLrel. 17, I
                                                                                                                                                                                         Complete
SEQUENCE
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                                                                                                                                                                                                                                               Genome Res. 0:0-0(2001).
EMBL; AE006281; AAK04541.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-IL1403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1360;
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Nature 406:959-964(2000).
EMBL; AE004532; AAG04381.1;
InterPro; IPR000259; Fimbrial.
Pfam: PF00419; Fimbrial; 1.
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Q914X7;
Q1-MAR-2001
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                 Similarity 35.: 6; Conservative
                                                                                                                                                                                      proteome.
251 AA;
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E 205 AA;
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                                                                                                                                                                               28744 MW;
                                              47.98;
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   Score 23; DB 2; Le
Pred. No. 1.1e+02;
0; Mismatches 11;
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Pred. No. 85;
0; Mismatches
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                                                                                                                                                                        A7E842DE042B03A1 CRC64;
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85;
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Query Match
Best Local Similarity
"Atches 5; Conserv
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Best Local
                                                                                       Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki Y., Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Nabekura T., Ishii S., Kawai Y., Salto K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.; NEDO human cDNA sequencing project."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

InterPro: IPR001230: Prenyltn.
PROSITE; PS00294; PRENYLATION; UNKNOWN_1.

SEQUENCE 892 AA: 102234 MW; 155C299D6944854D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9H8E6;
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE-PLACENTA;
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN, CILIARY
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (CDNA FLJ13704
                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chopin A., Bolotin A., Sorokin A., Ehrlich S.D., Chopin M.-C.; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF323670; ARX08356.1; -. SEQUENCE 251 AA; 28744 MW; A7E842DE042B03A1 CRC64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001
01-JUN-2001
01-JUN-2001
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"Analysis of six prophages in Lactococcus lactis I
genetic structure of temperate and virulent phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=21113149; PubMed=11160885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
04 FIS, CLONE PLACE2000274, WEAKLY SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                 Chordata;
Primates;
                             47.9%;
27.8%;
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35.3%;
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17,
17,
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     Score 23; DB 4; L
Pred. No. 4.1e+02;
3; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23; DB
Pred. No. 1.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A7E842DE042B03A1
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                                            Length 892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 251;
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IL1403: different
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Conservative

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Gaps